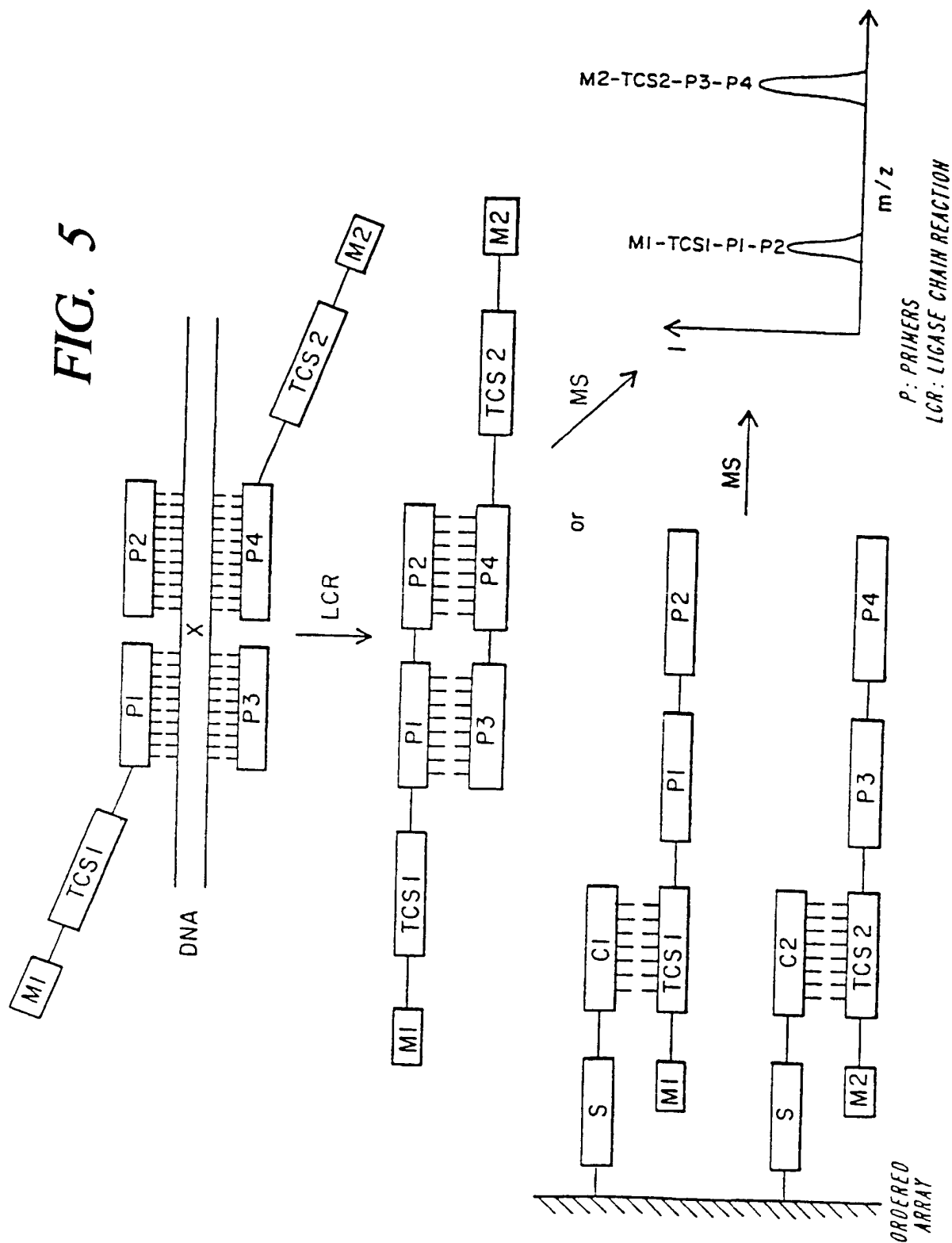
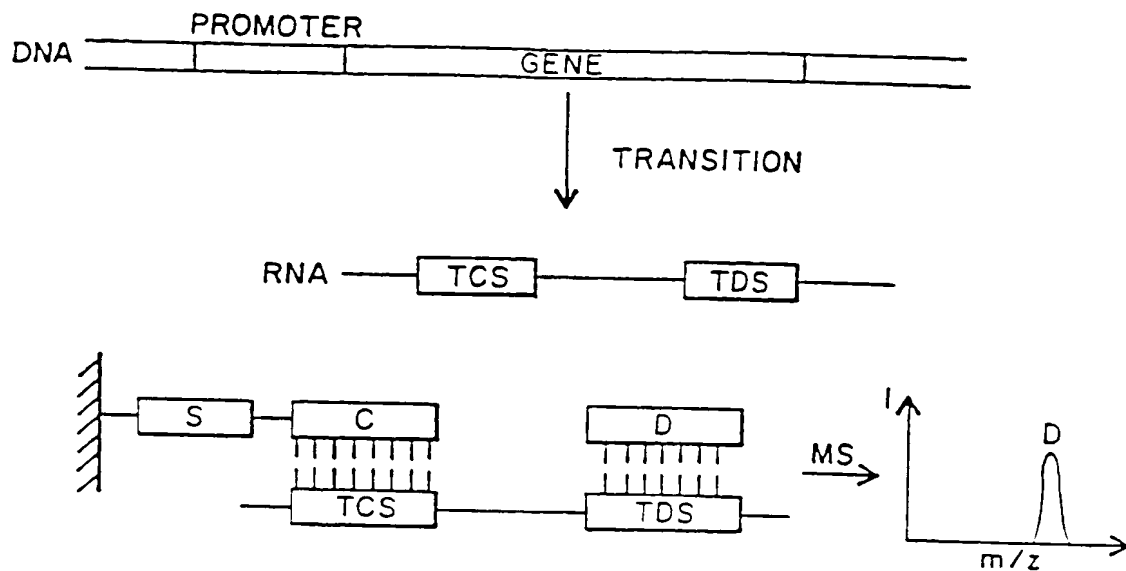
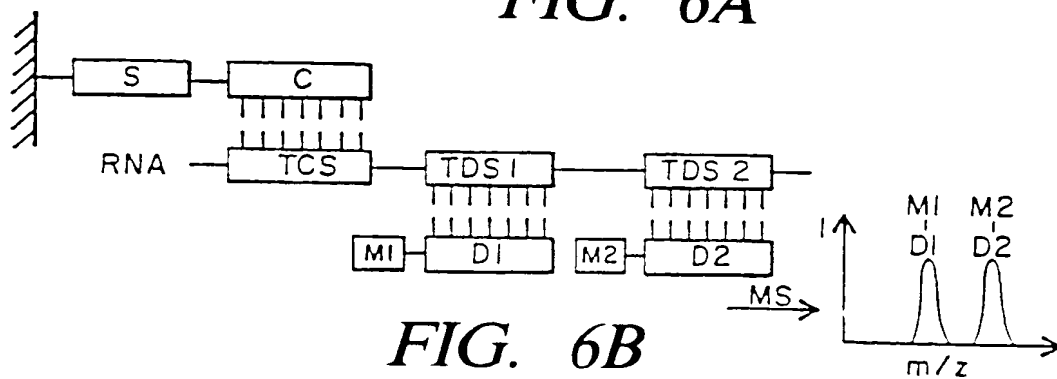
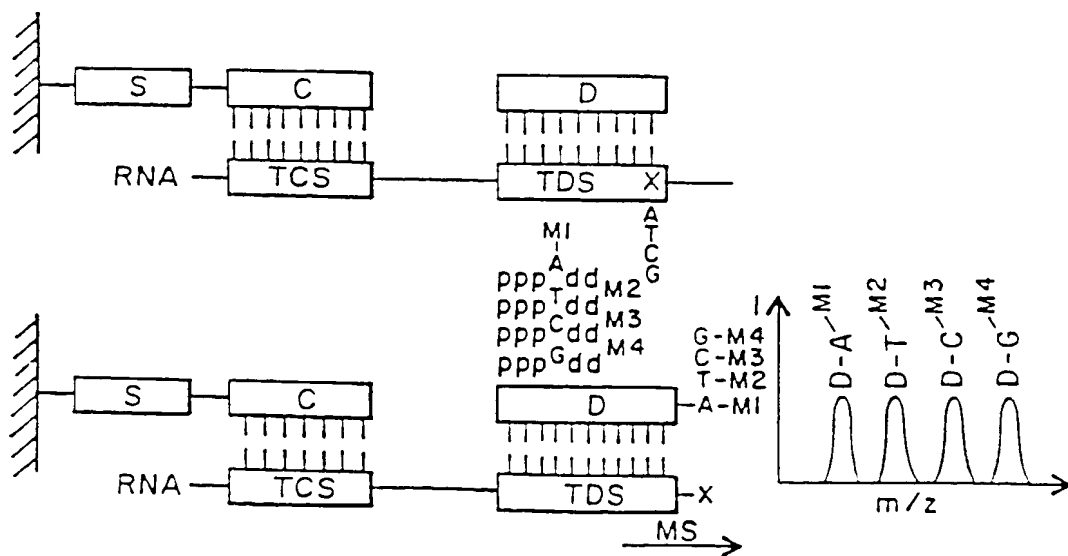


FIG. 5



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*FIG. 6A**FIG. 6B**FIG. 6C*

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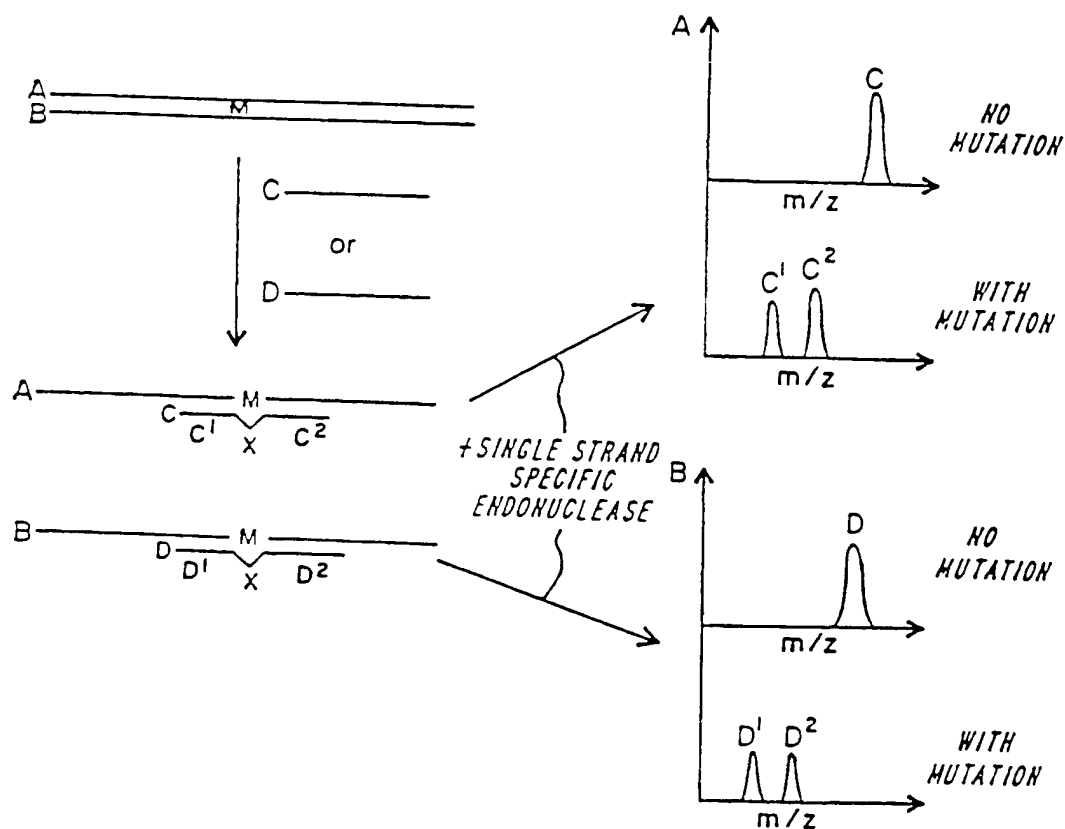
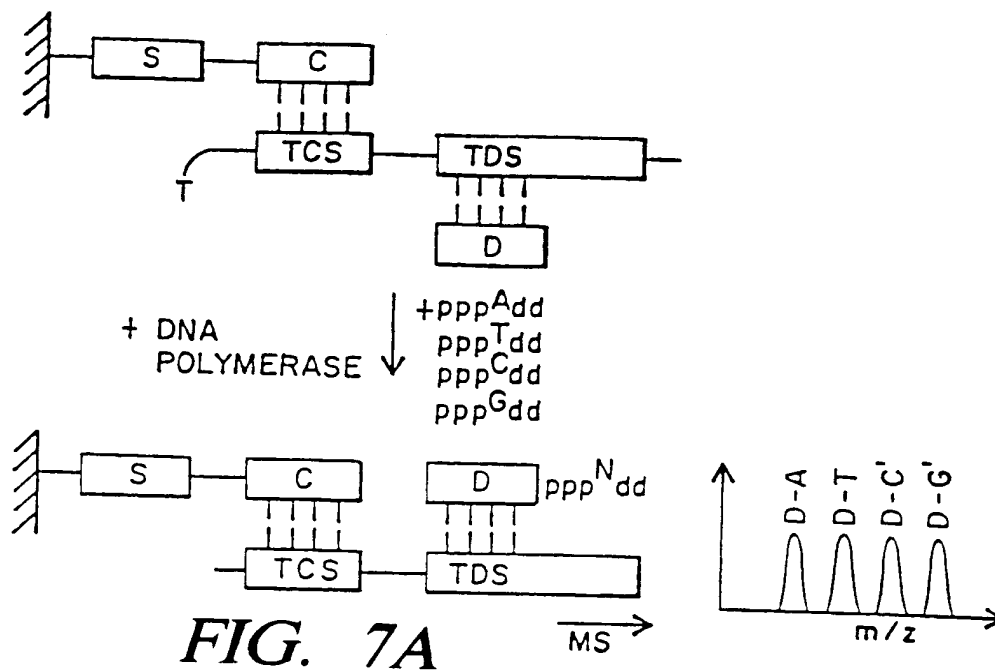


FIG. 7B

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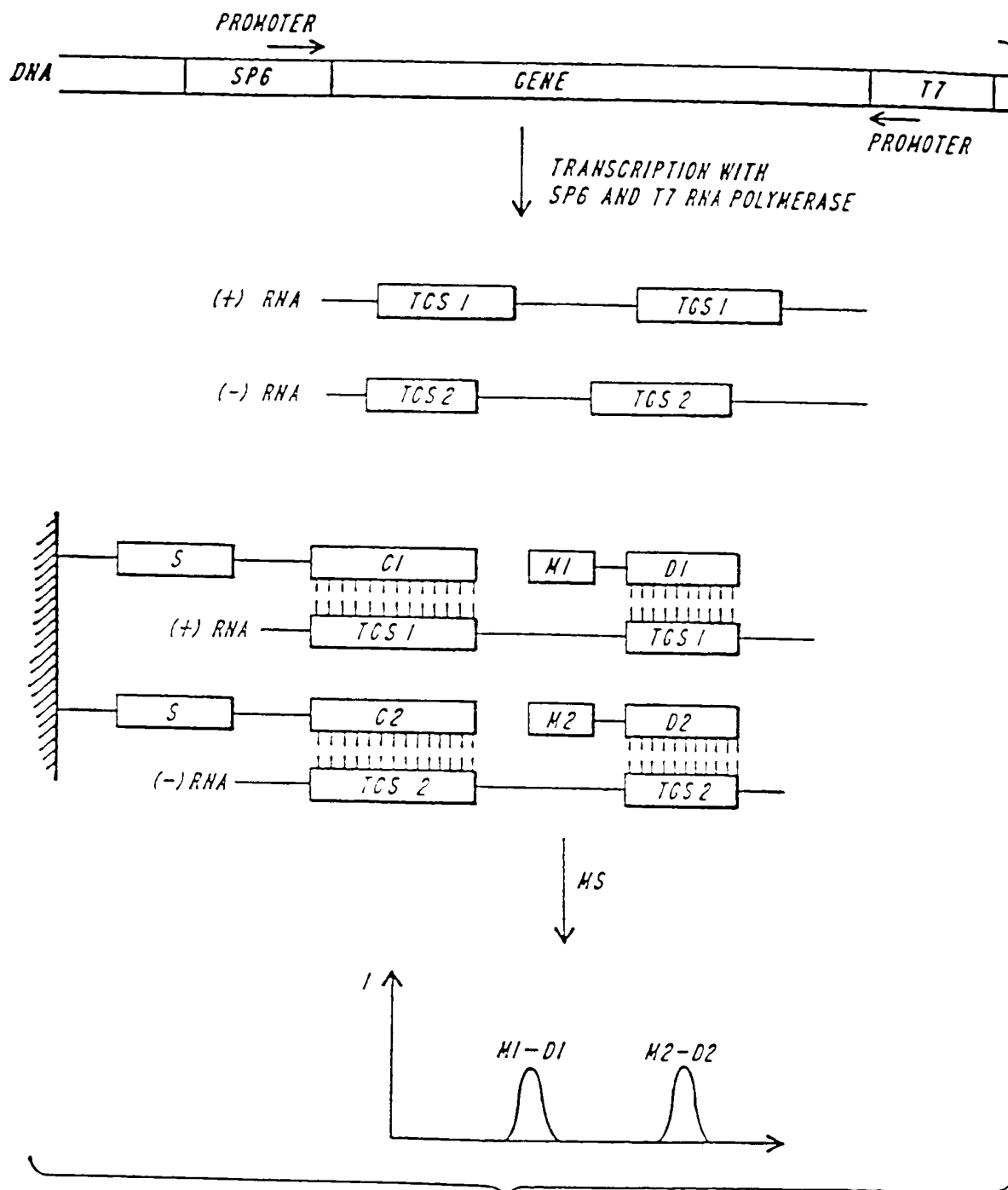
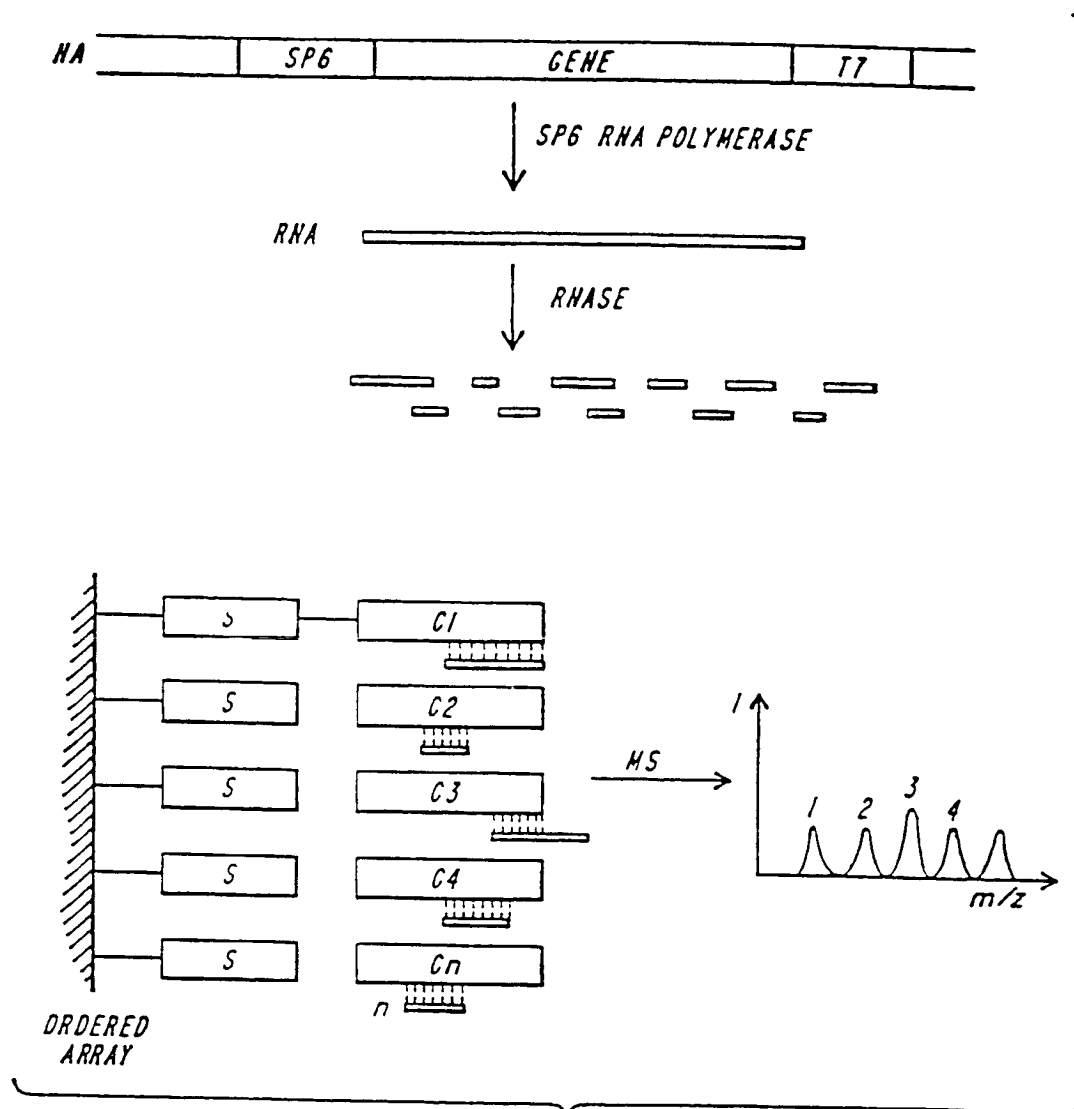
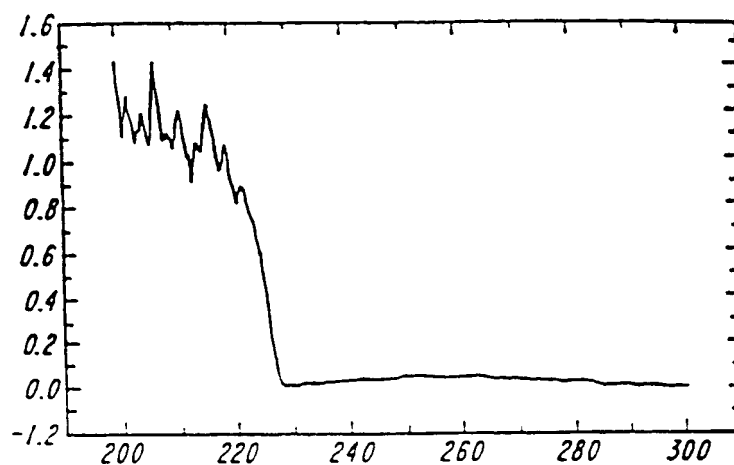
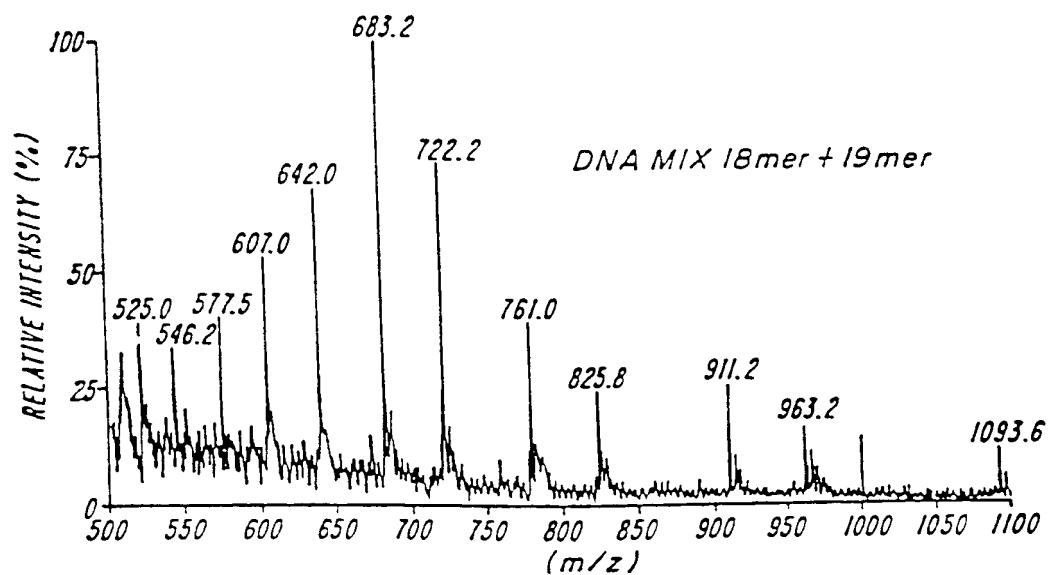


FIG. 8

**FIG. 9**

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*FIG. 10B**FIG. 12A*

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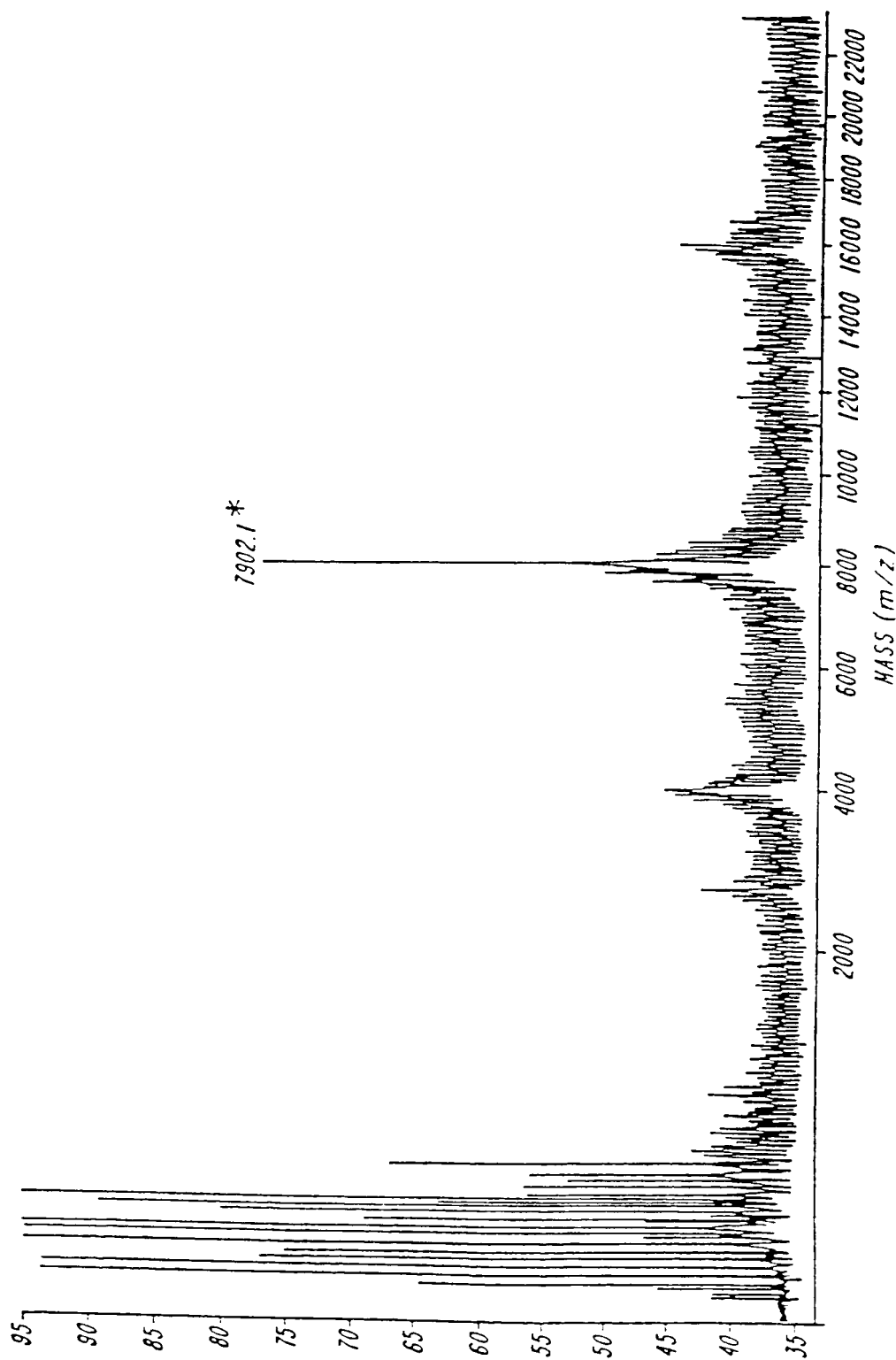
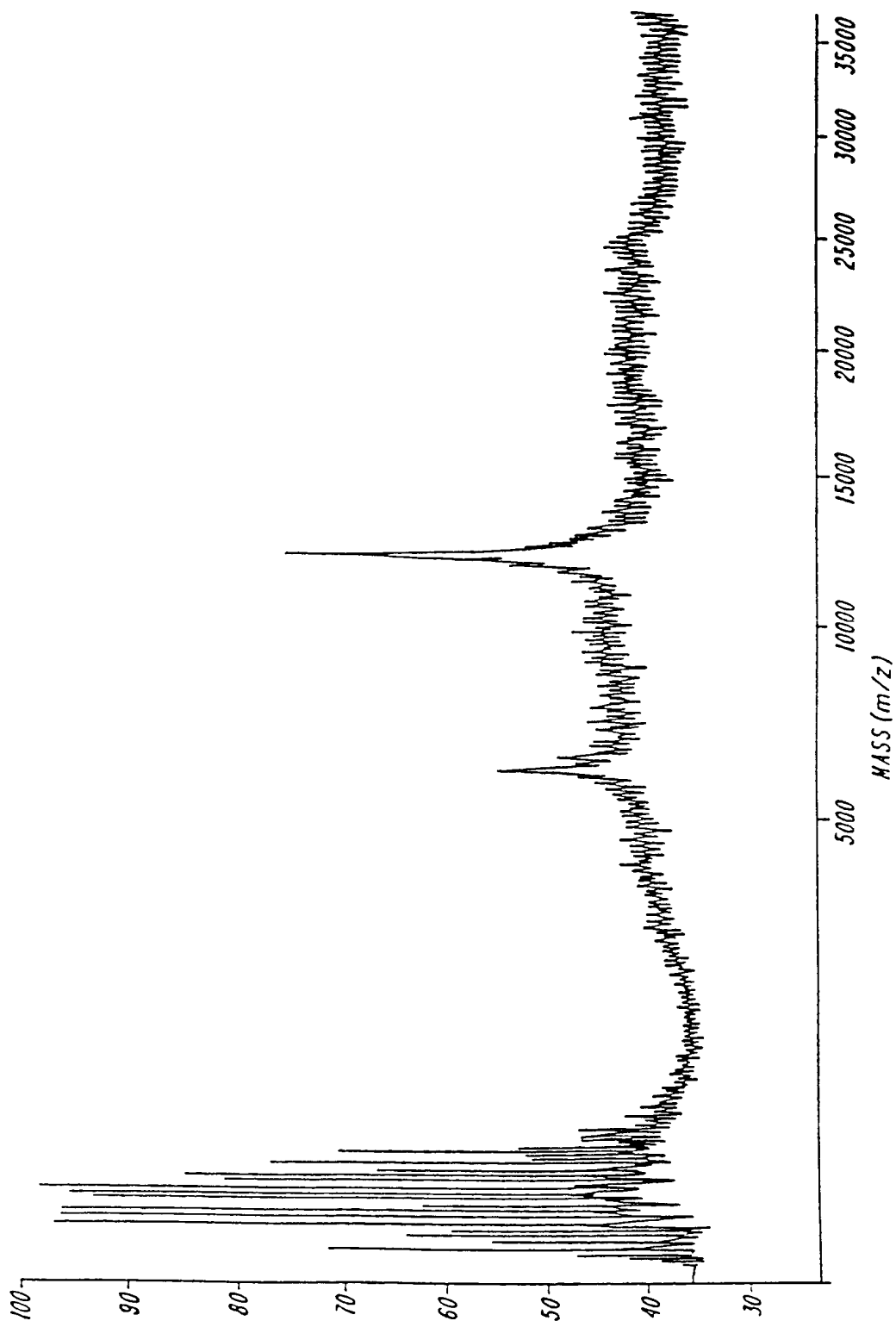


FIG. 10C

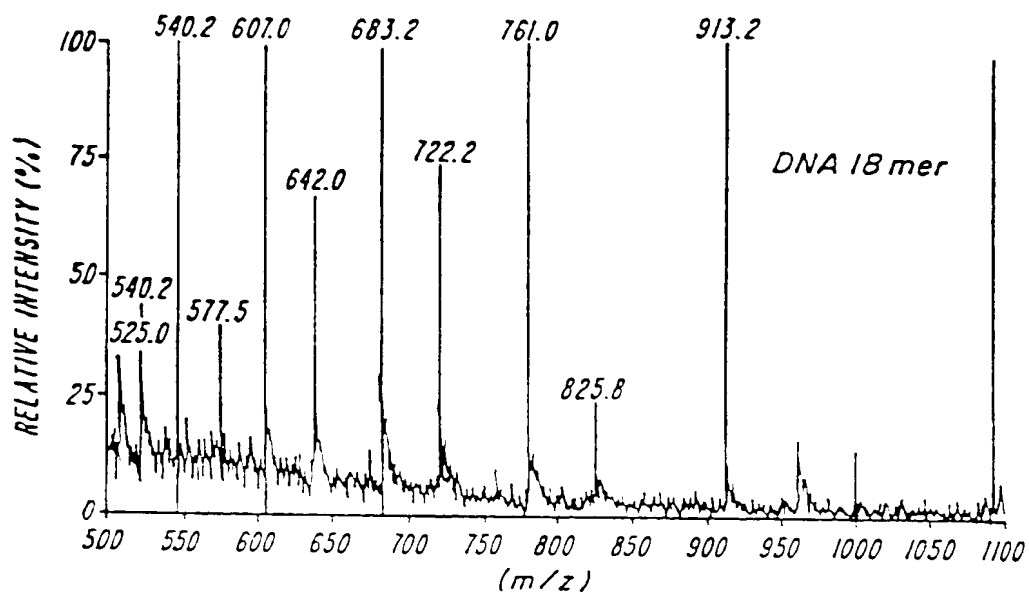
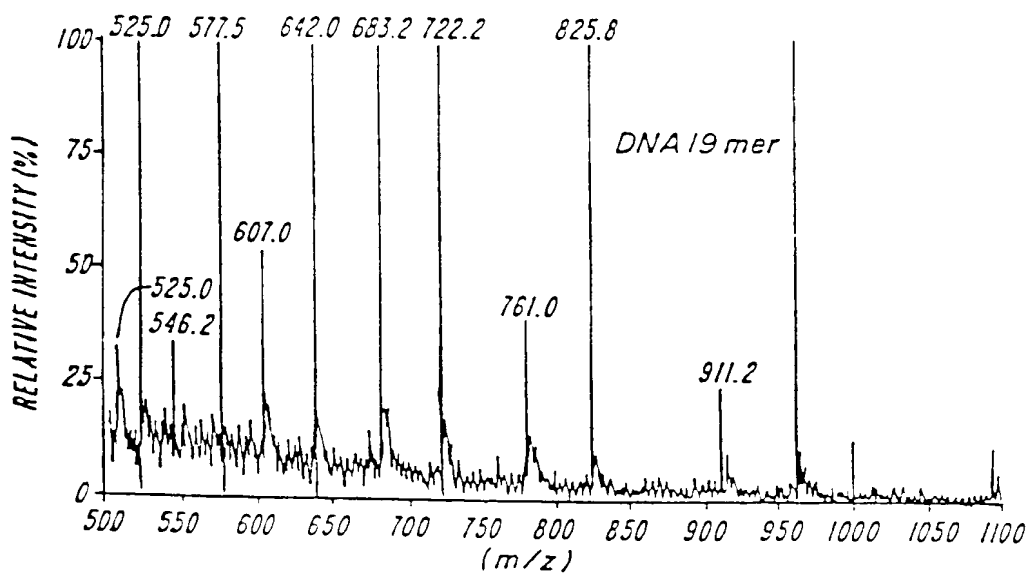
SUBSTITUTE SHEET (RULE 26)

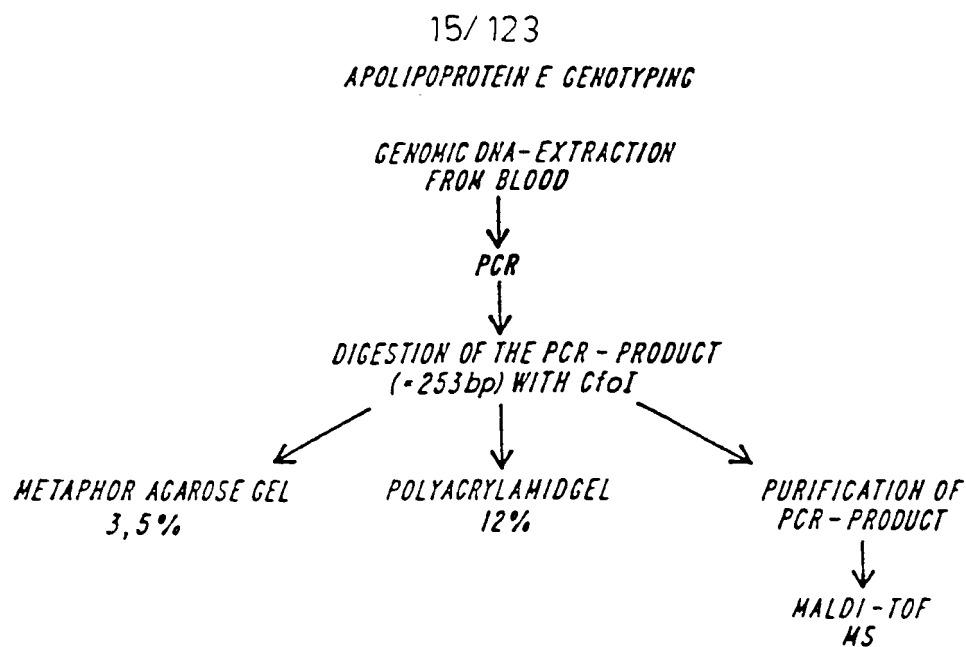
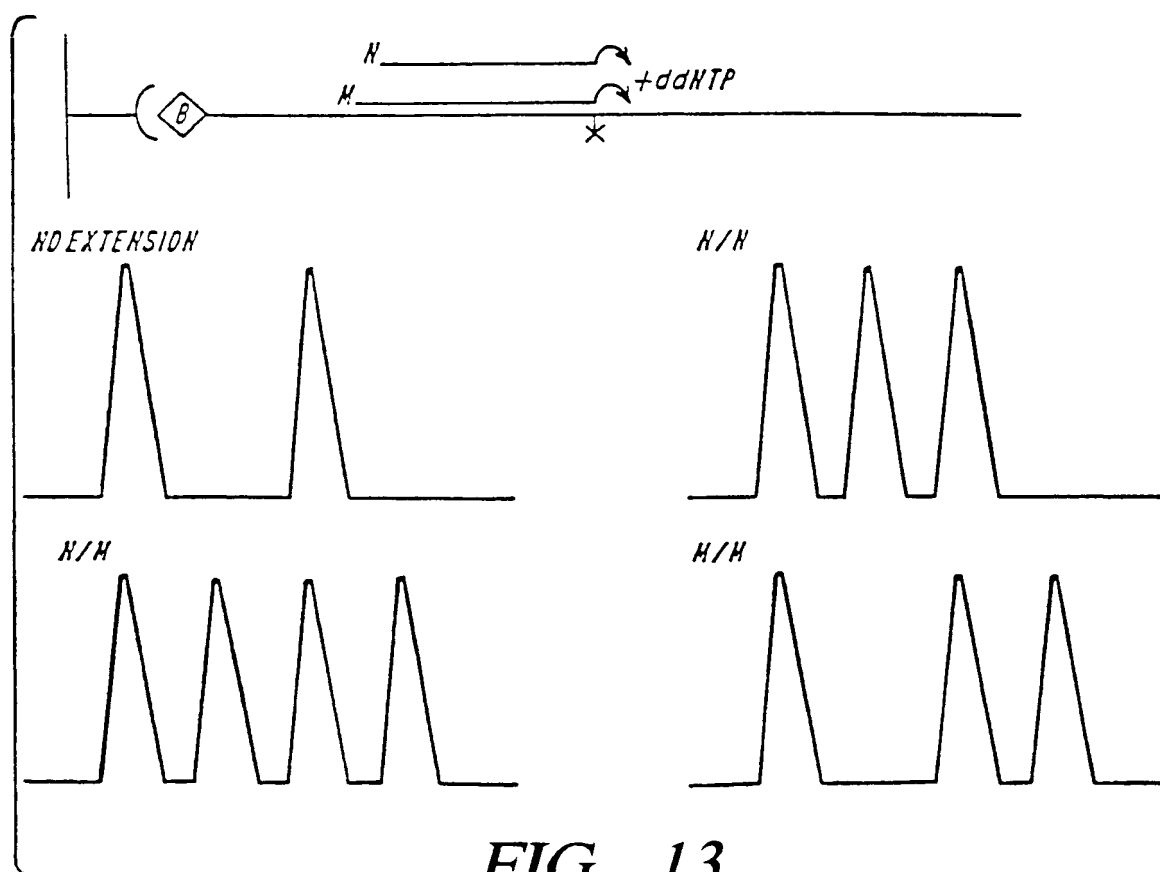
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**FIG. 11**

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**FIG. 12B****FIG. 12C**

**FIG. 19****FIG. 13**

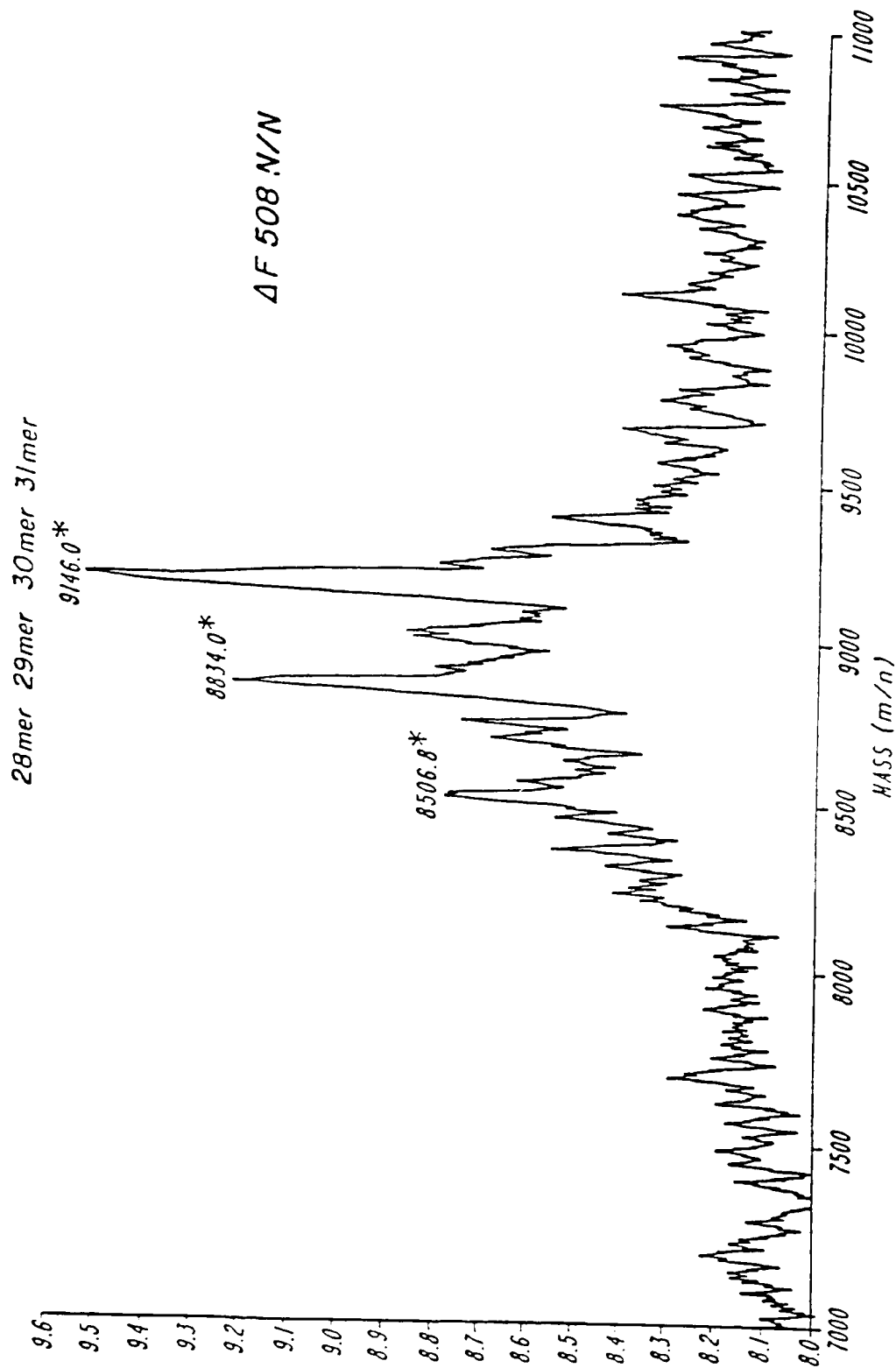


FIG. 14

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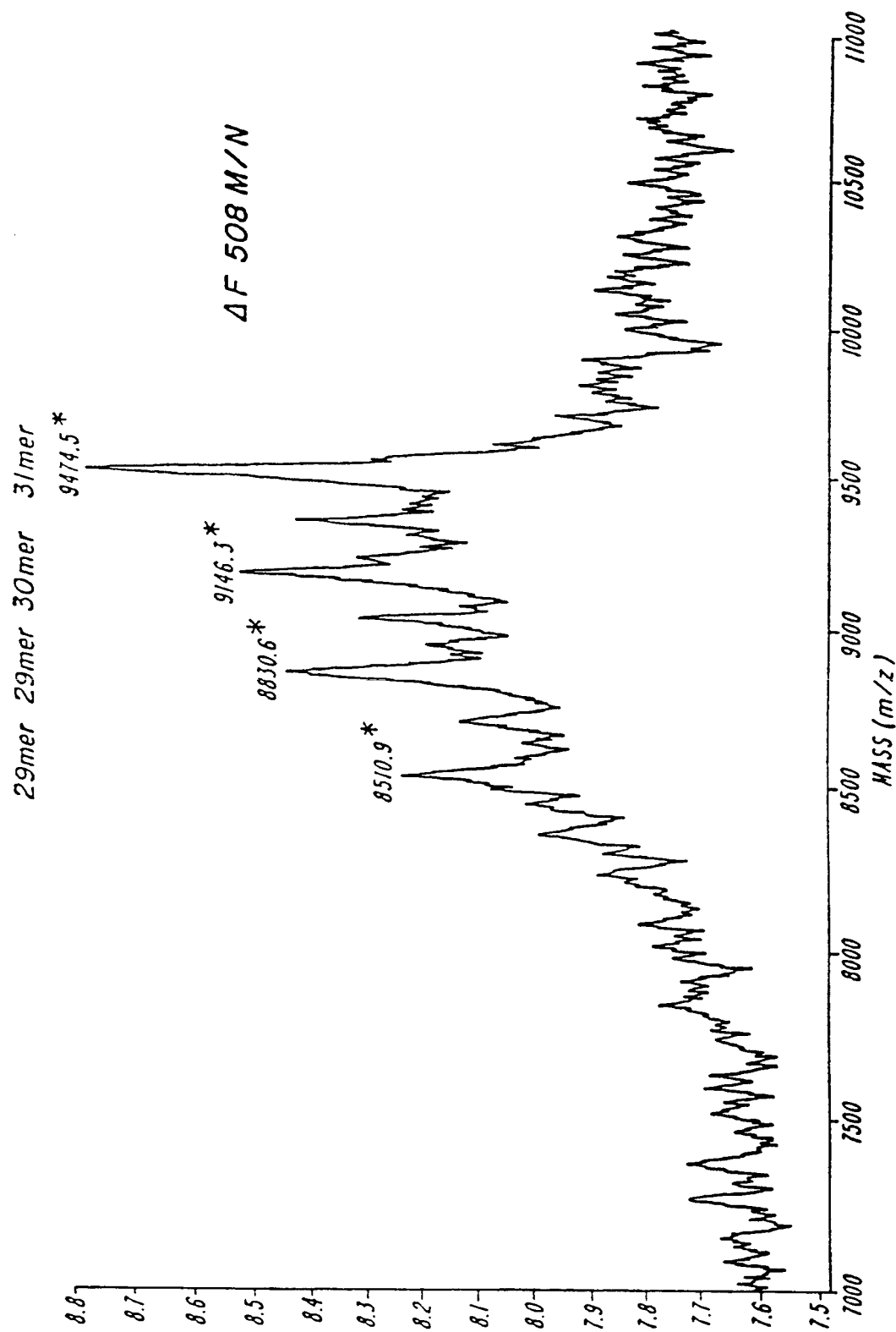


FIG. 15

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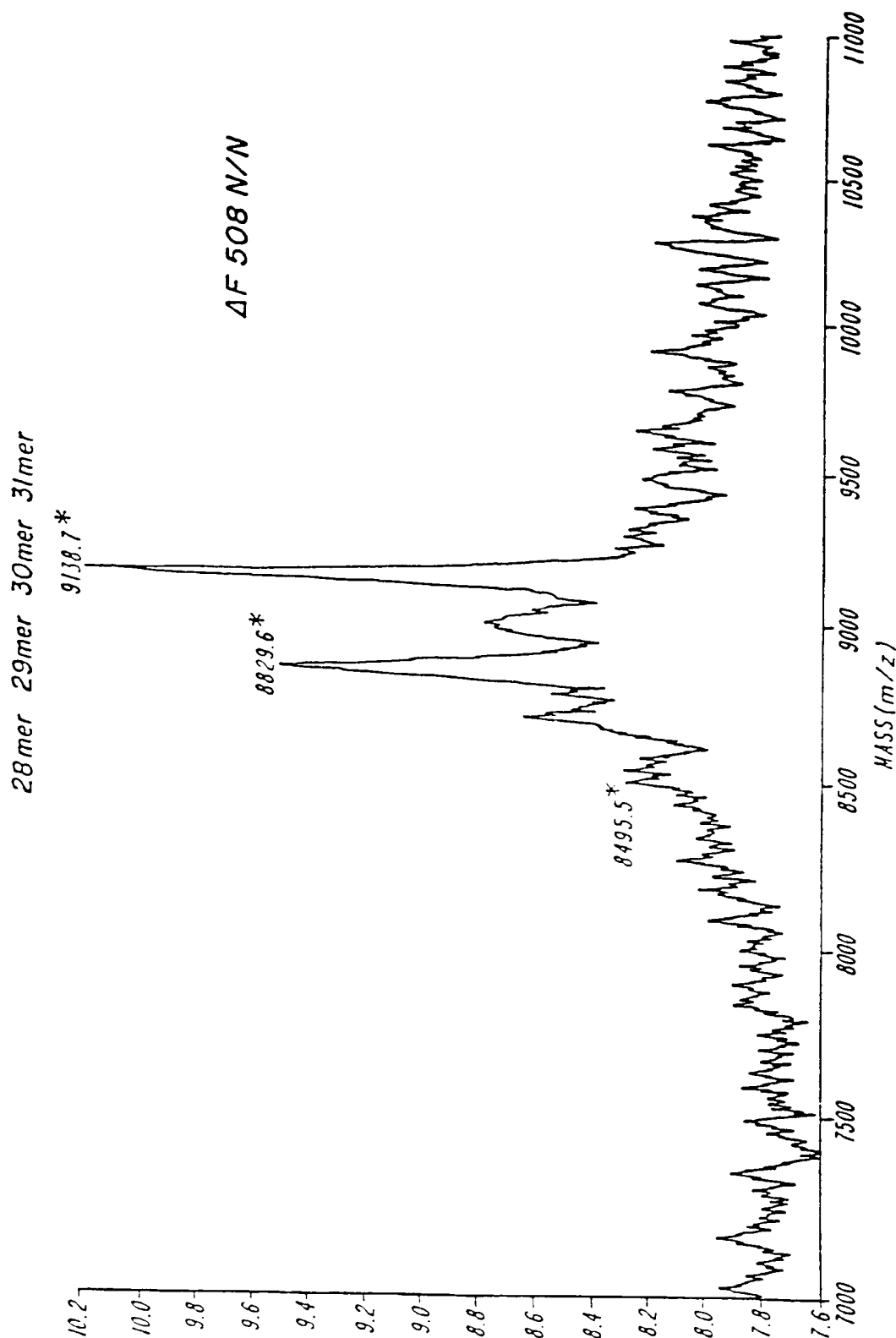


FIG. 16

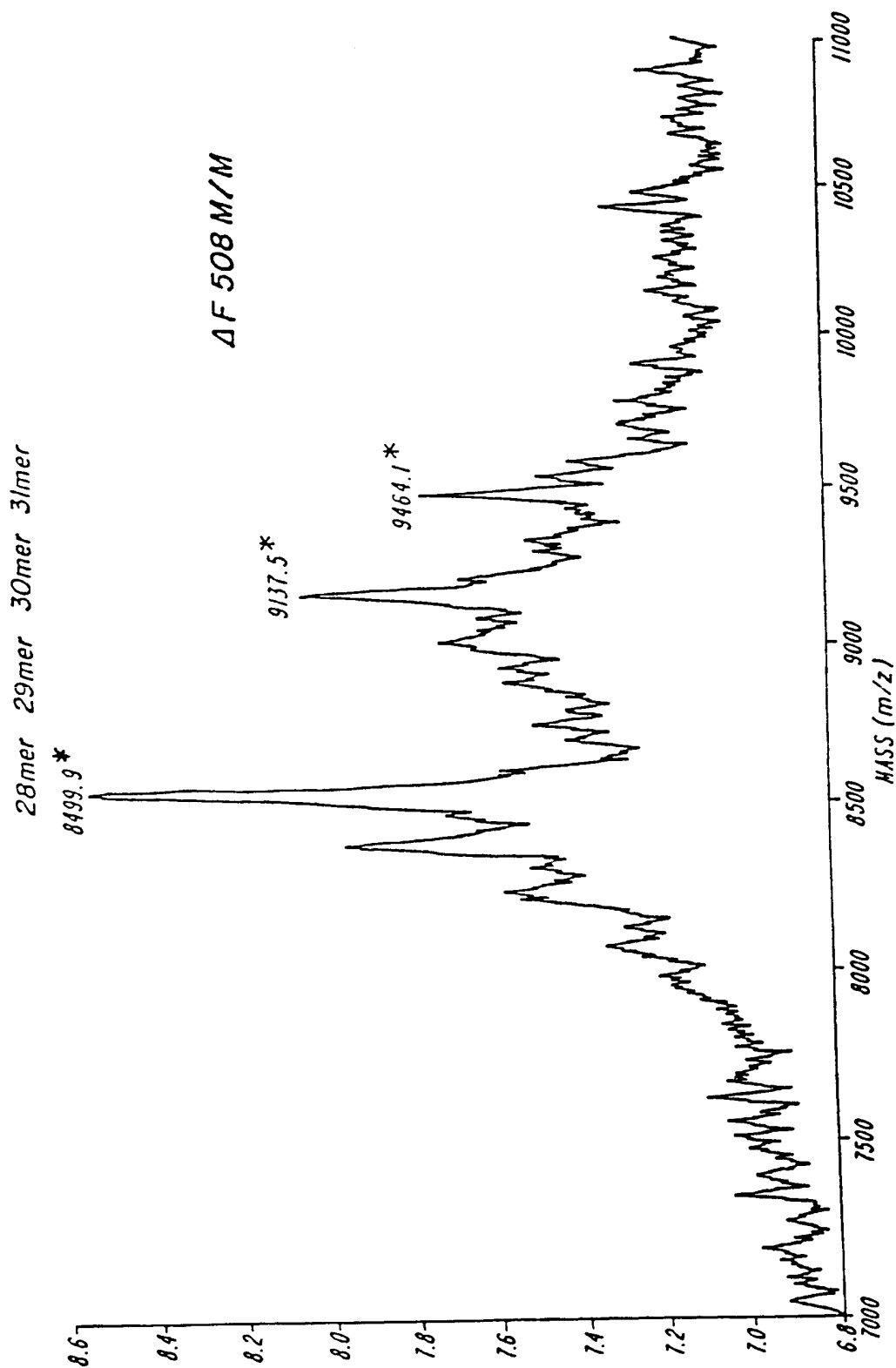


FIG. 17

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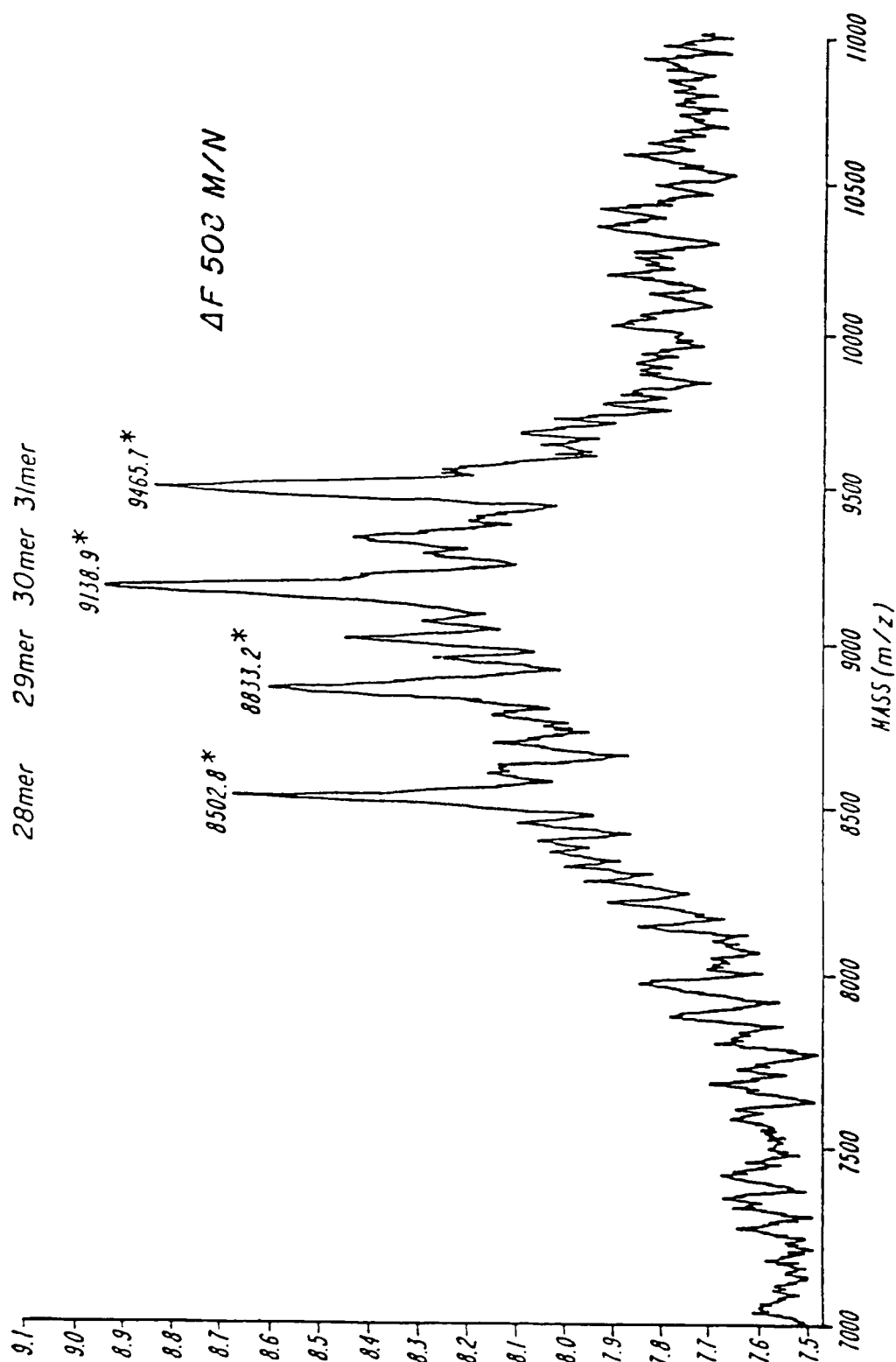
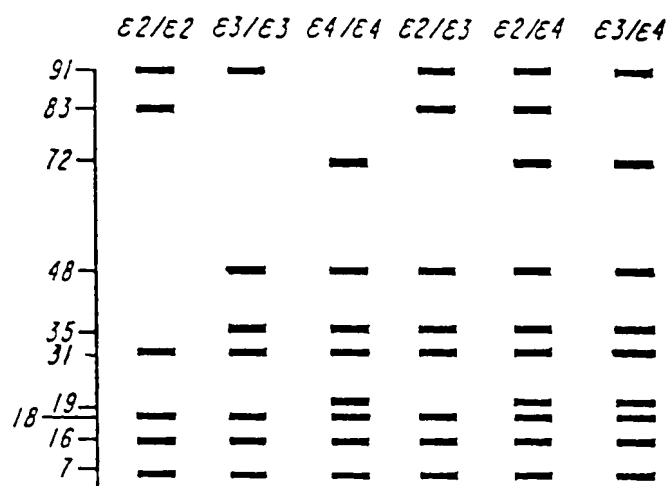


FIG. 18

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*FIG. 21A*

MetaPhor Agarose Gel
3, 5 %

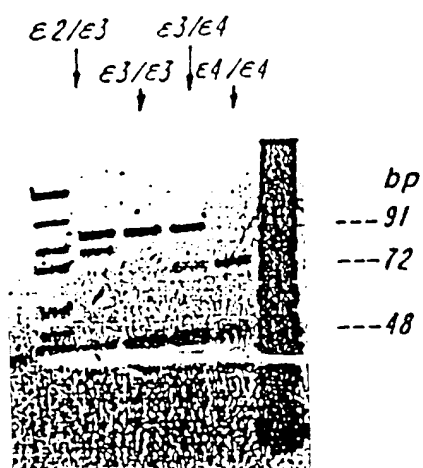


FIG. 21B

Polyacrylamidgel
12 %



FIG. 21C

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MOLECULAR WEIGHT OF THE VARIABLE FRAGMENTS IN Da:

			$\epsilon 2/\epsilon 2$	$\epsilon 3/\epsilon 3$	$\epsilon 4/\epsilon 4$	$\epsilon 2/\epsilon 3$	$\epsilon 2/\epsilon 4$	$\epsilon 3/\epsilon 4$
91 bp	SENSE	28421	X	X		X	X	X
	ANTISENSE	27864						
83bp	SENSE	25747	X			X	X	
	ANTISENSE	25591						
72bp	SENSE	22440			X		X	X
	ANTISENSE	21494						
48bp	SENSE	14844		X	X	X	X	X
	ANTISENSE	14857						
35bp	SENSE	10921		X	X	X	X	X
	ANTISENSE	10751						

FIG. 22A

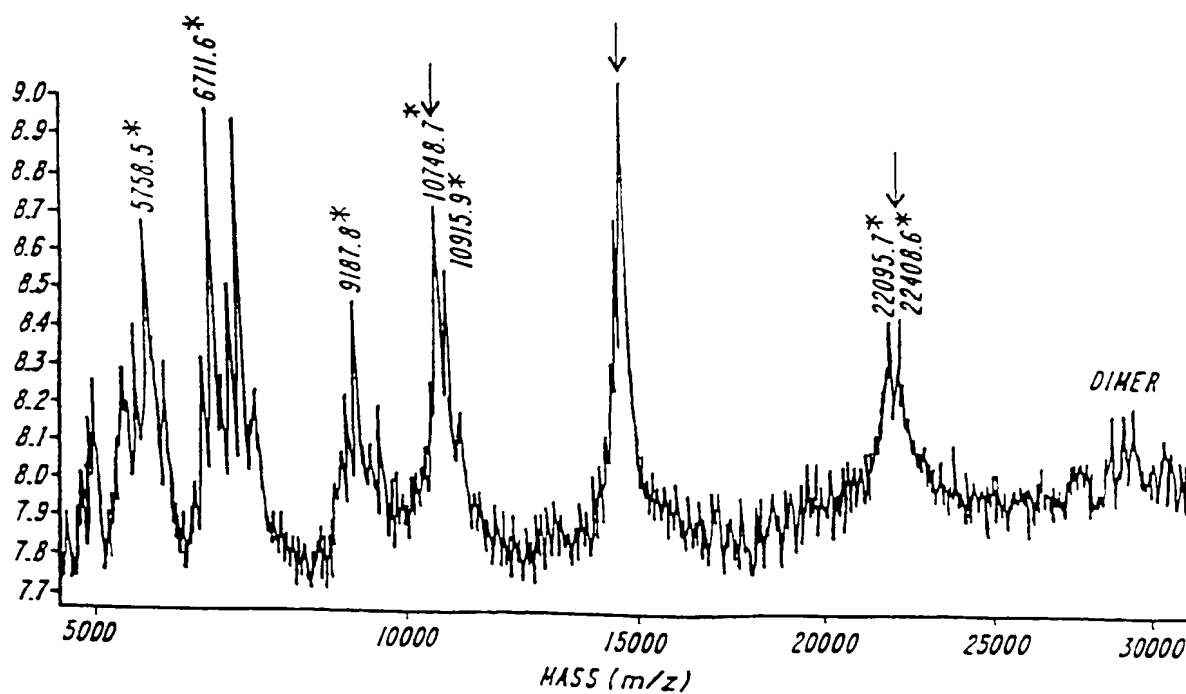


FIG. 22B

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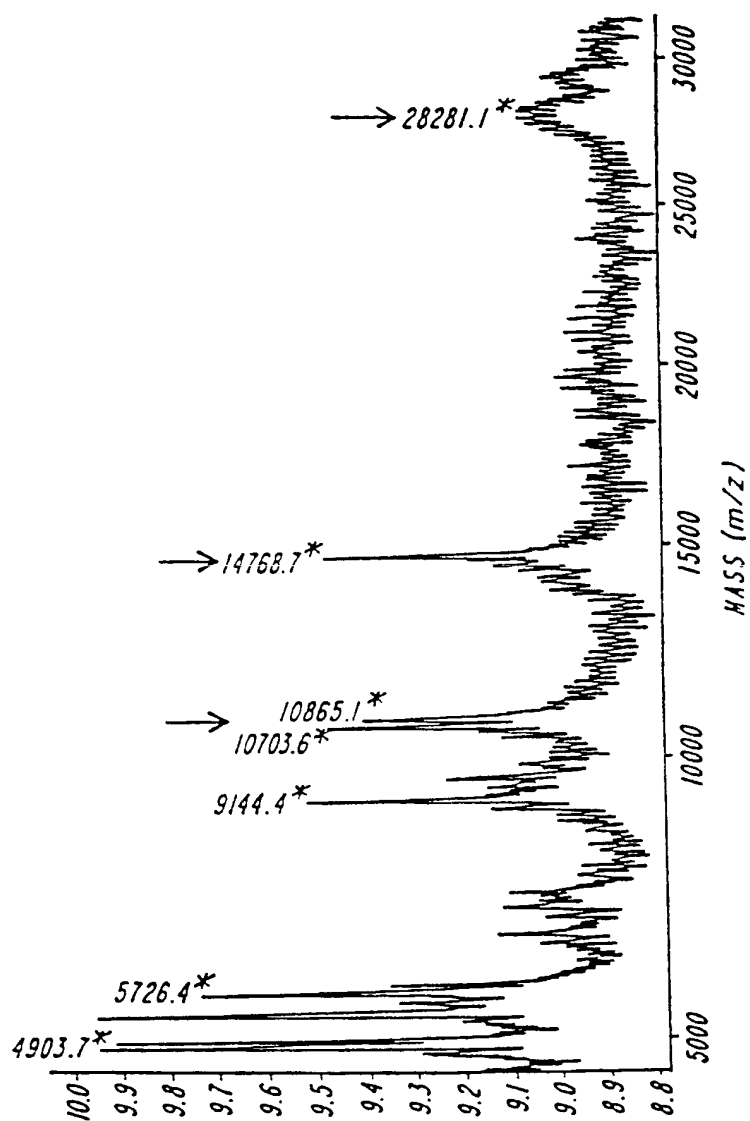


FIG. 23A

SUBSTITUTE SHEET (RULE 26)

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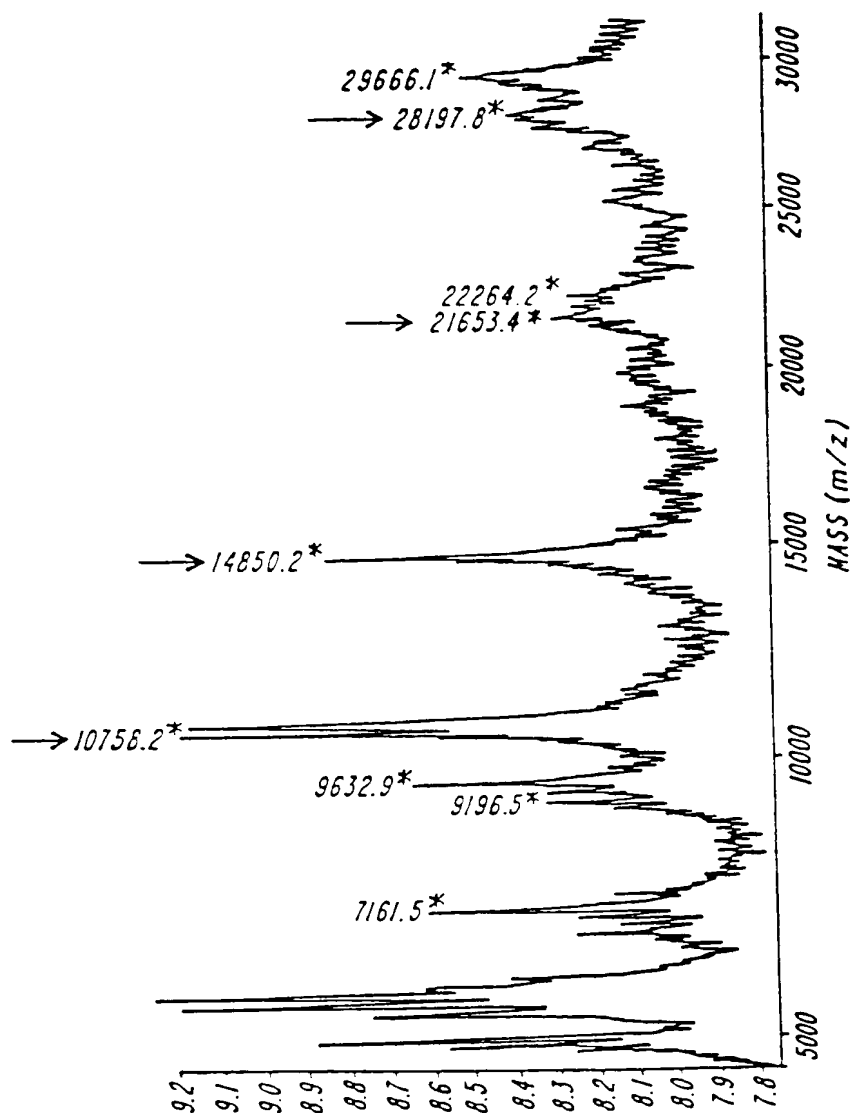
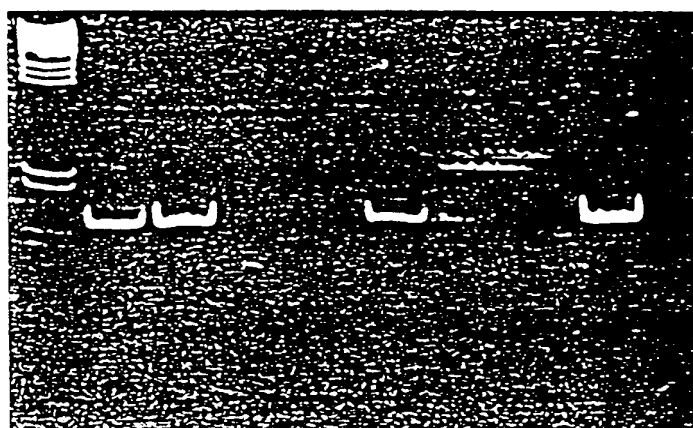


FIG. 23B

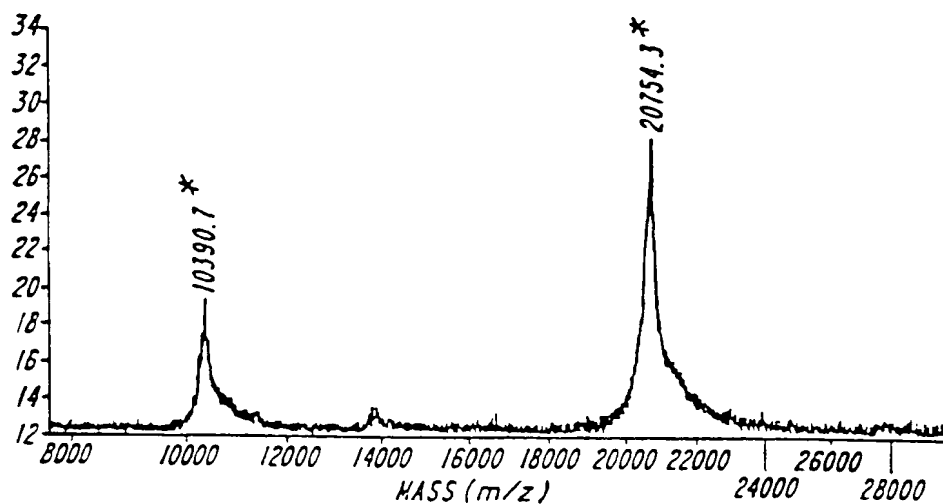
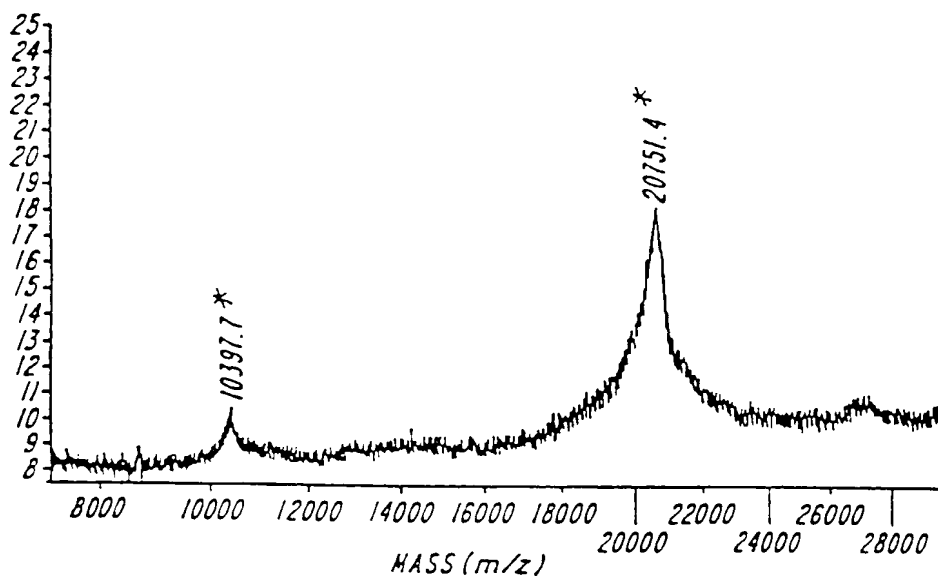
SUBSTITUTE SHEET (RULE 26)



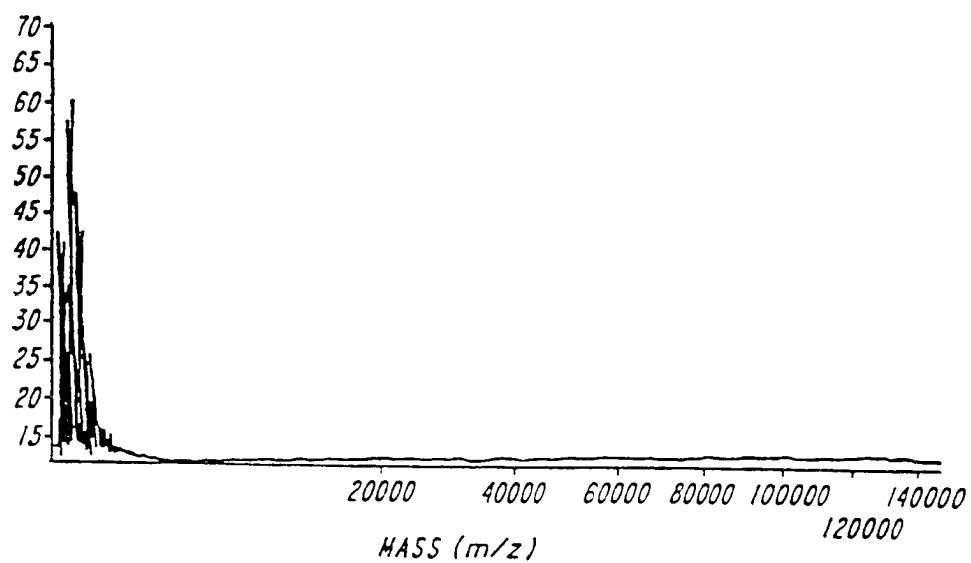
M 1 2 3 4 5 6

FIG. 24

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*FIG. 25A**FIG. 25B*

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*FIG. 25C*

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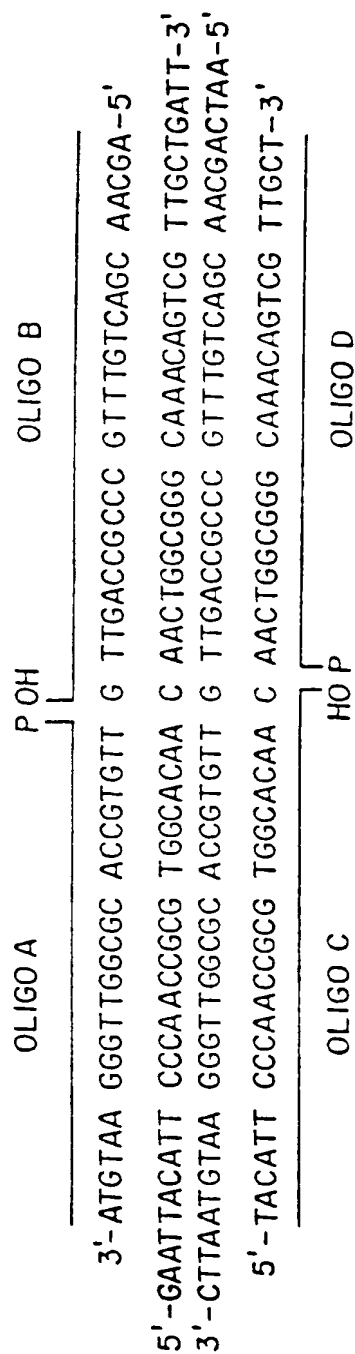


FIG. 26

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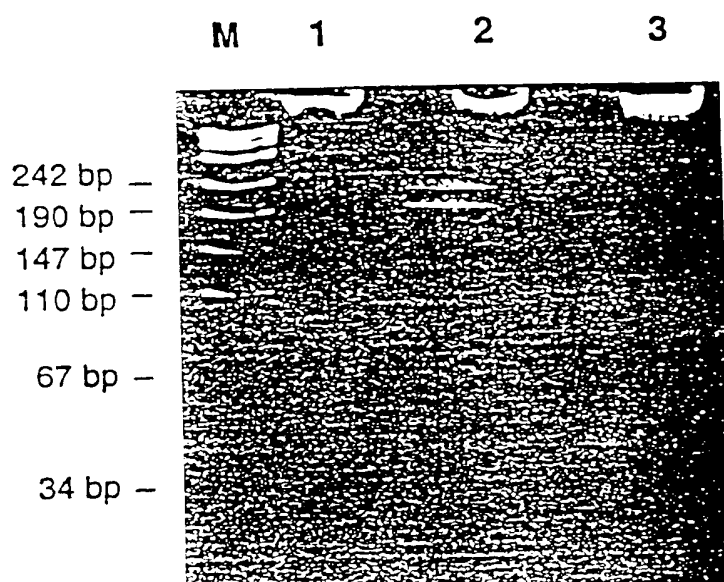
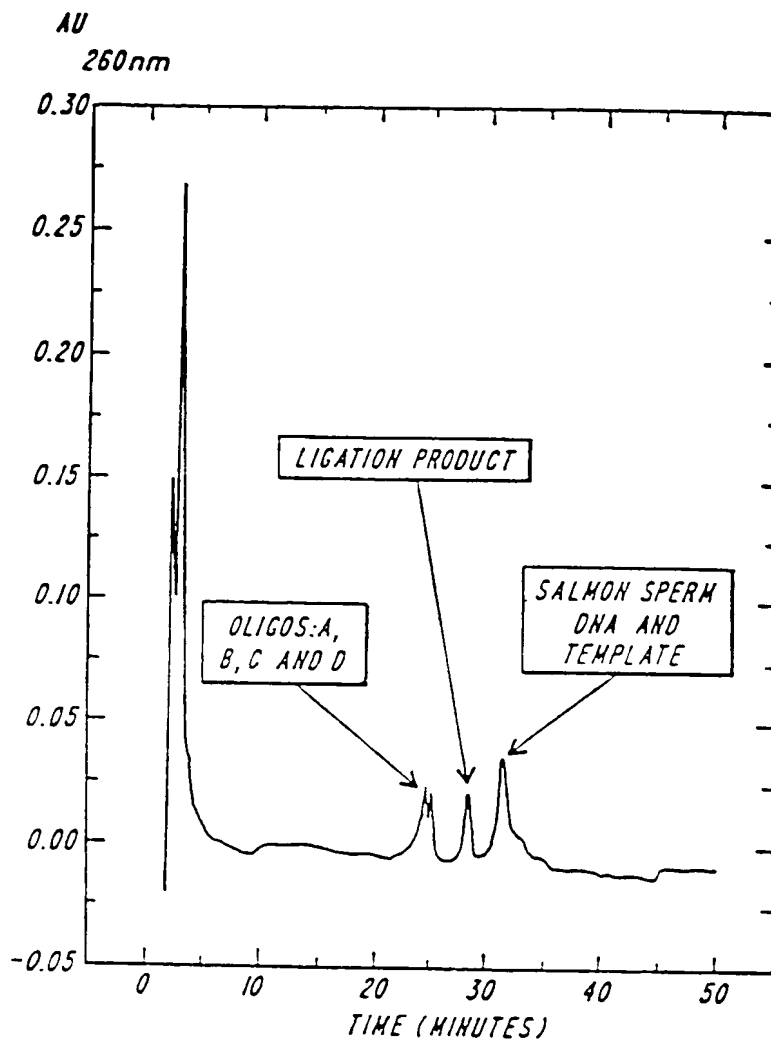
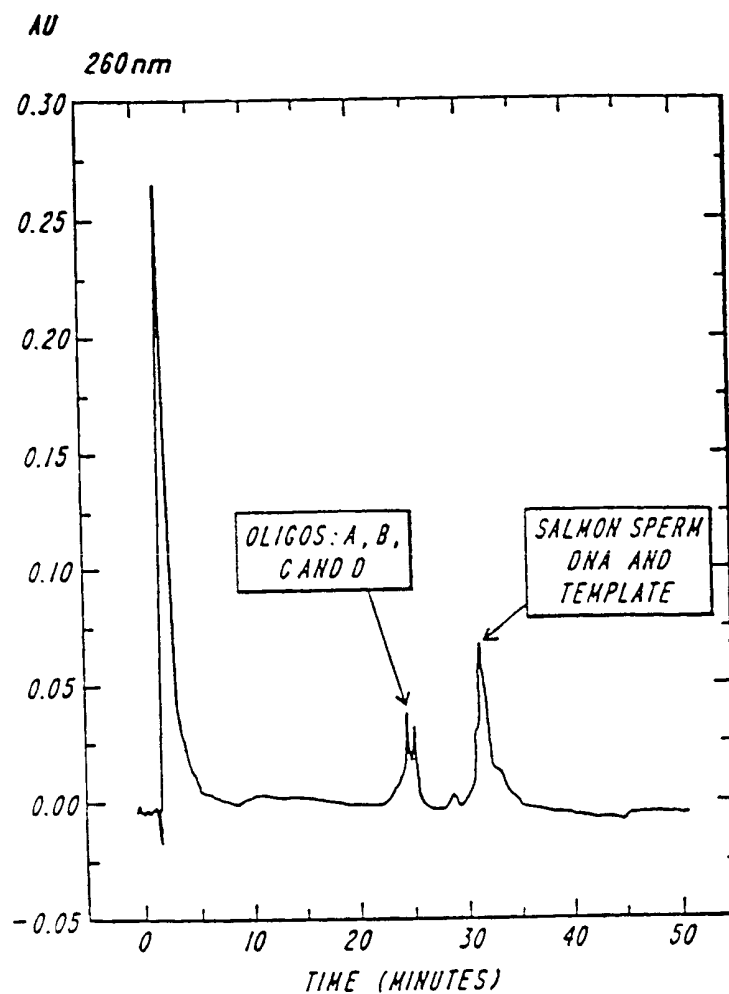


FIG. 27

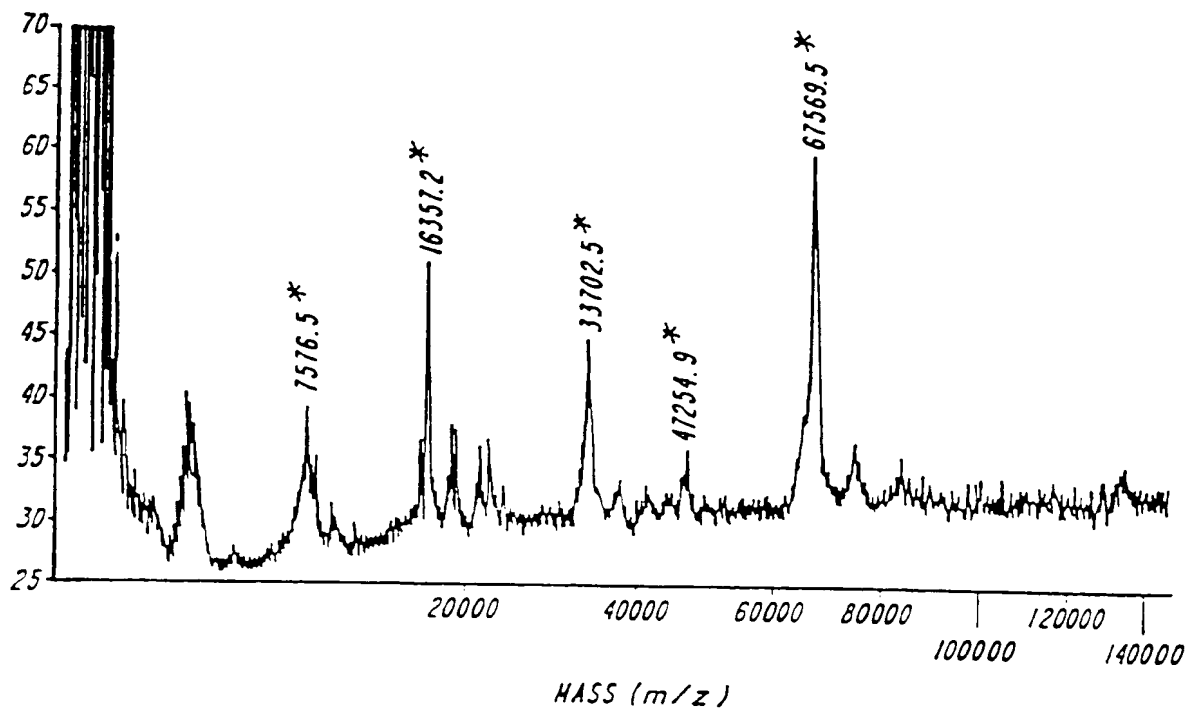
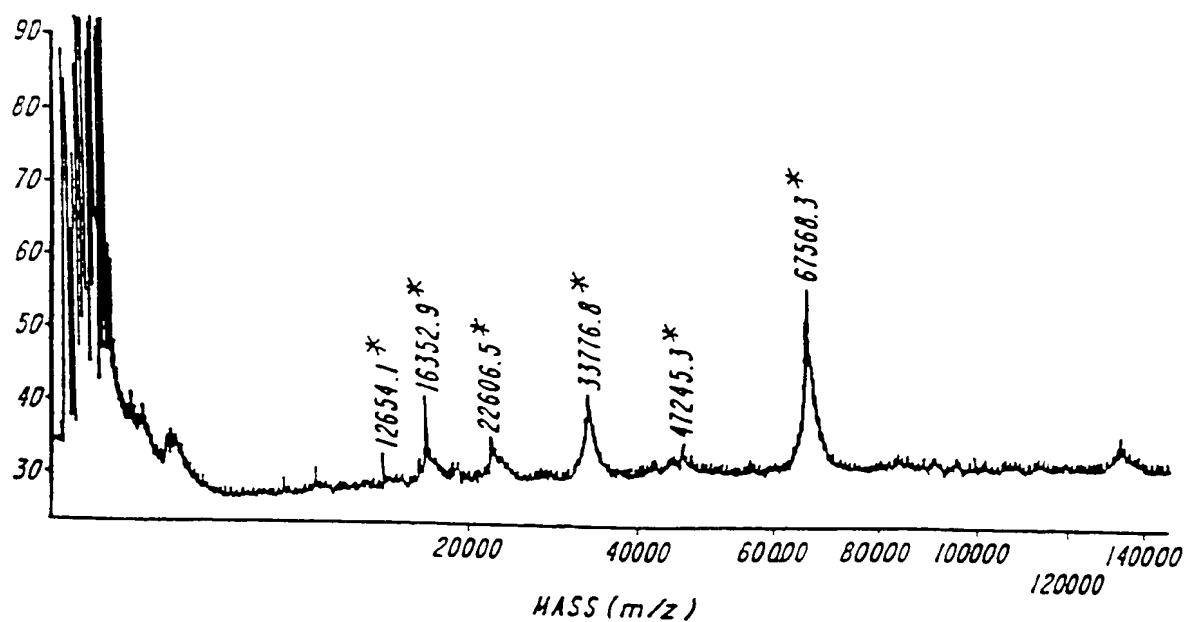
SUBSTITUTE SHEET (RULE 26)

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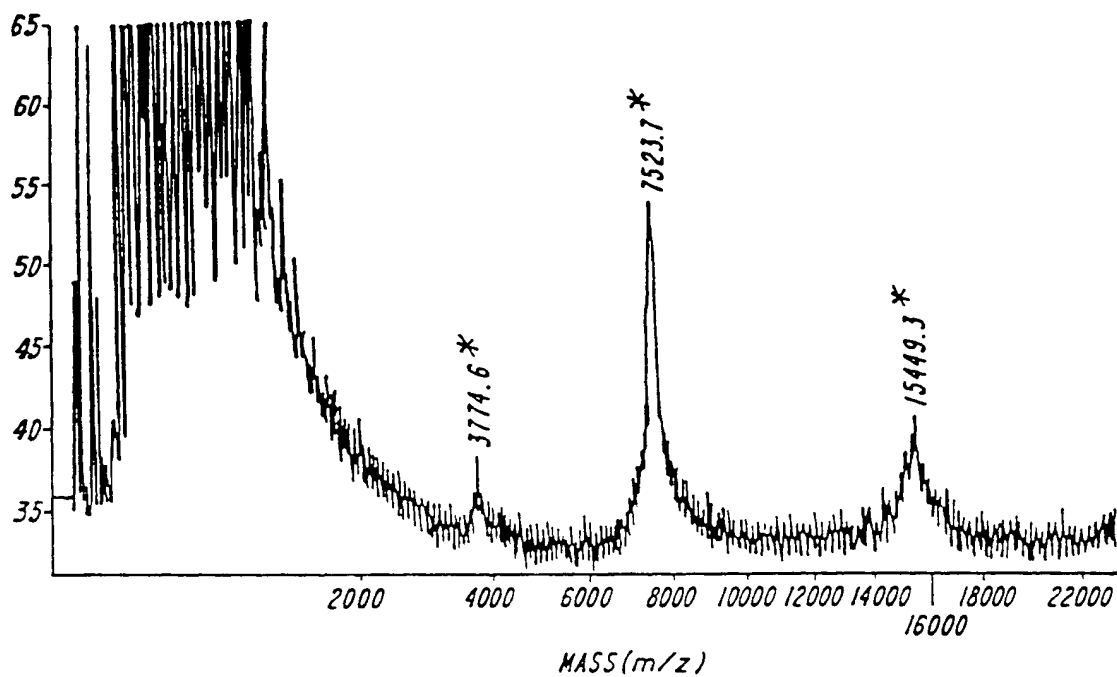
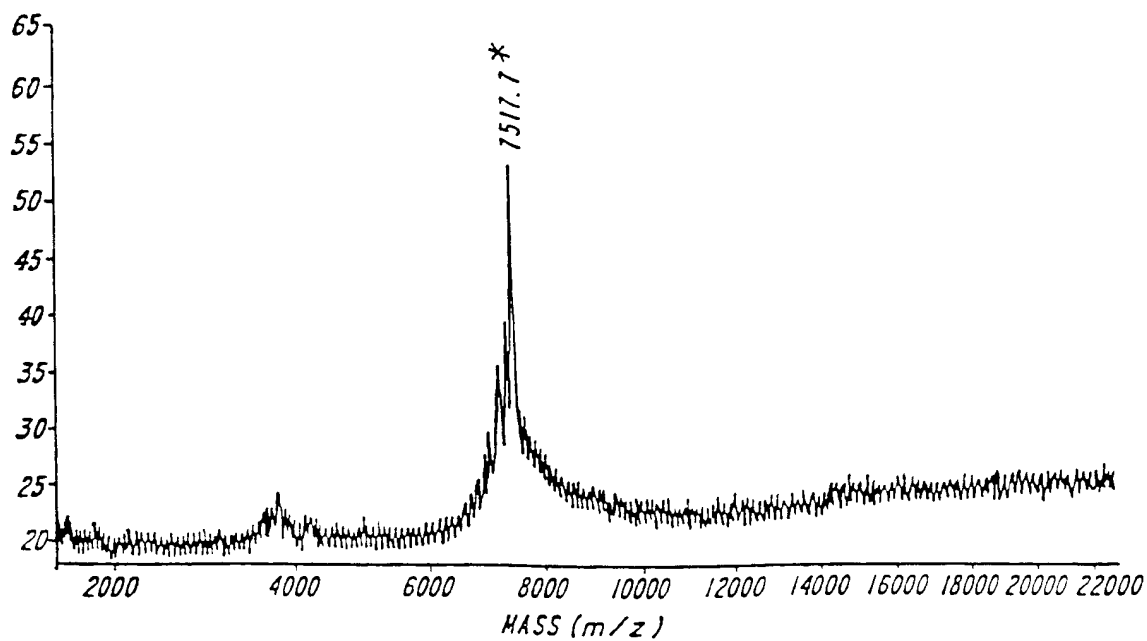
**FIG. 28**

**FIG. 29**

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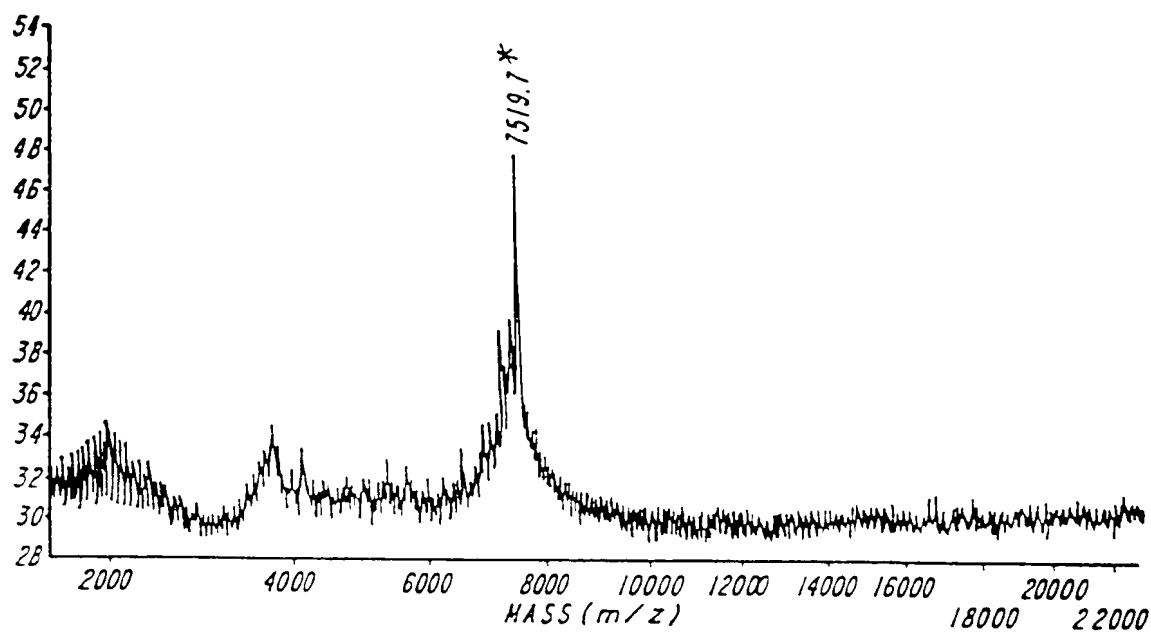
**FIG. 30A****FIG. 30B**

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*FIG. 31A**FIG. 31B*

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*FIG. 32*

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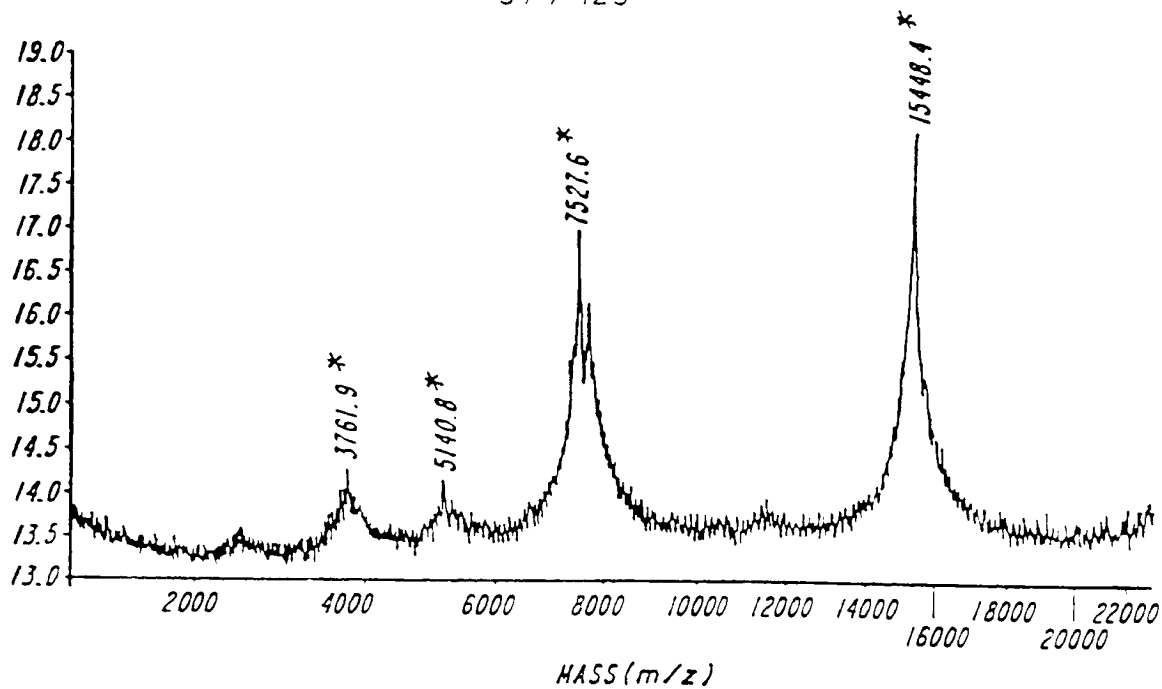


FIG. 33A

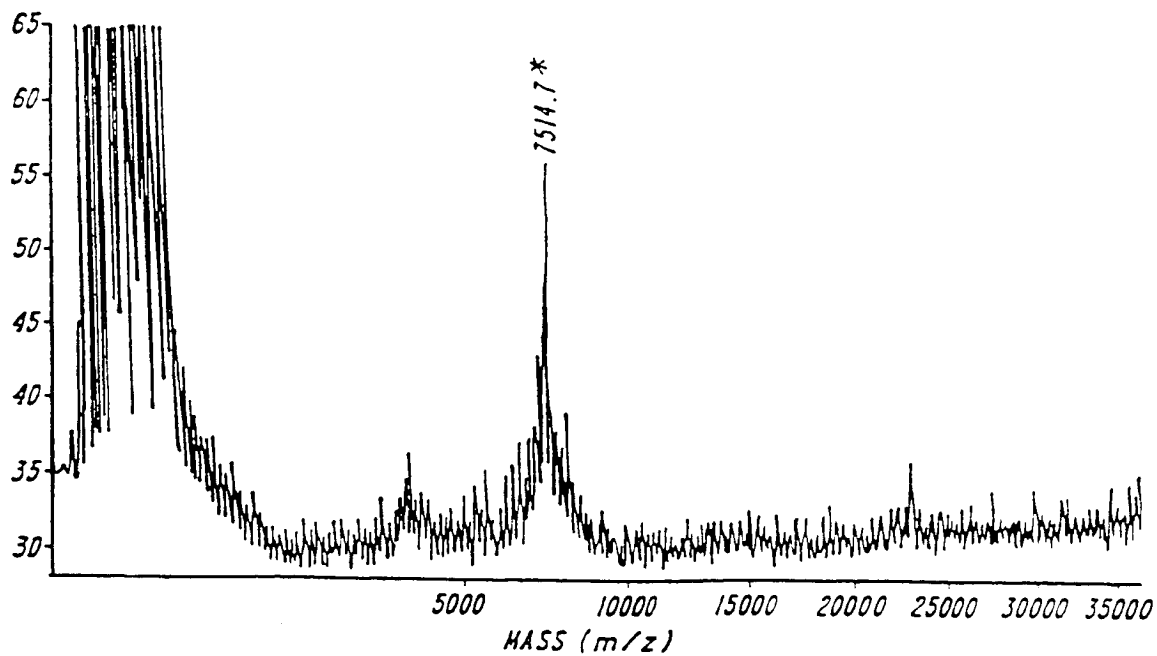


FIG. 33B

SUBSTITUTE SHEET (RULE 26)

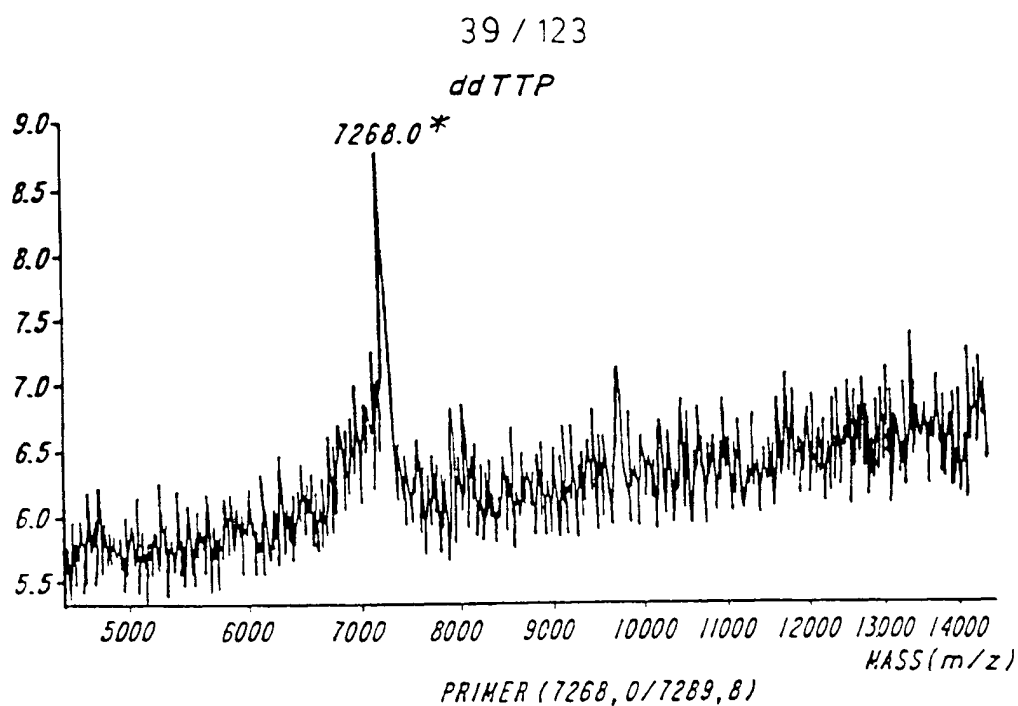
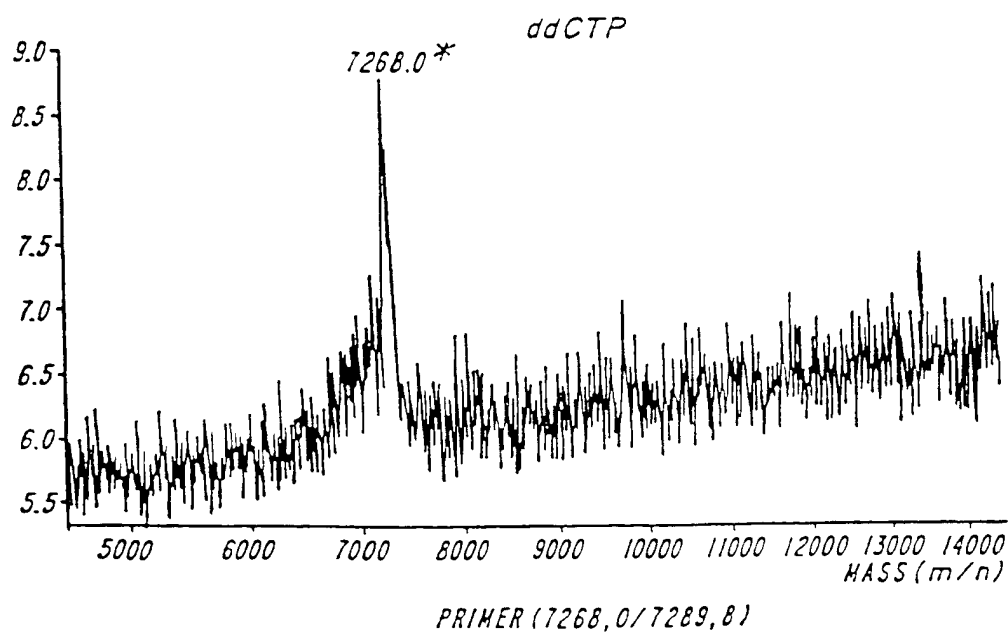
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506507508
IleIlePhe
ACCATTAAGAAATATCATCTTTGGTGTTTCCATGATGAATATAGAAGCGTCATC
primer ACCACAAAGGATACTACTTATATC (7289,8)
wildtype TAGAAACCCACAAAGGATACTACTTATATC (8846,8)
ΔF508 TA---ACCACAAAGGATACTACTTATATC (7891,2)
ΔI507 TAG---AAACCACAAAGGATACTACTTATATC (8846,8)

FIG. 34A

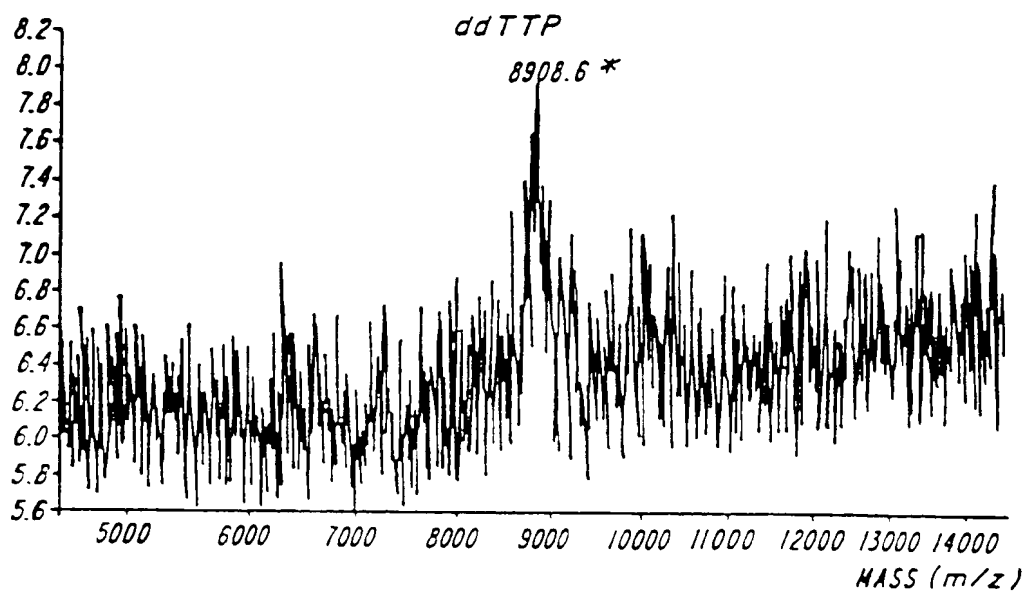
506507508
IleIlePhe
ACCATTAAGAAATATCATCTTTGGTGTTTCCATGATGAATATAGAAGCGTCATC
primer ACCACAAAGGATACTACTTATATC (7289,8)
wildtype CTTTATAGTAGAAACCCACAAAGGATACTACTTATATC (11612,6)
ΔF508 CTTTATAGTA---ACCACAAAGGATACTACTTATATC (10657,0)
ΔI507 CTTTATAG---AAACCACAAAGGATACTACTTATATC (10666,0)
506Ser CGTAGAAACCCACAAAGGATACTACTTATATC (9465,2)

FIG. 34B

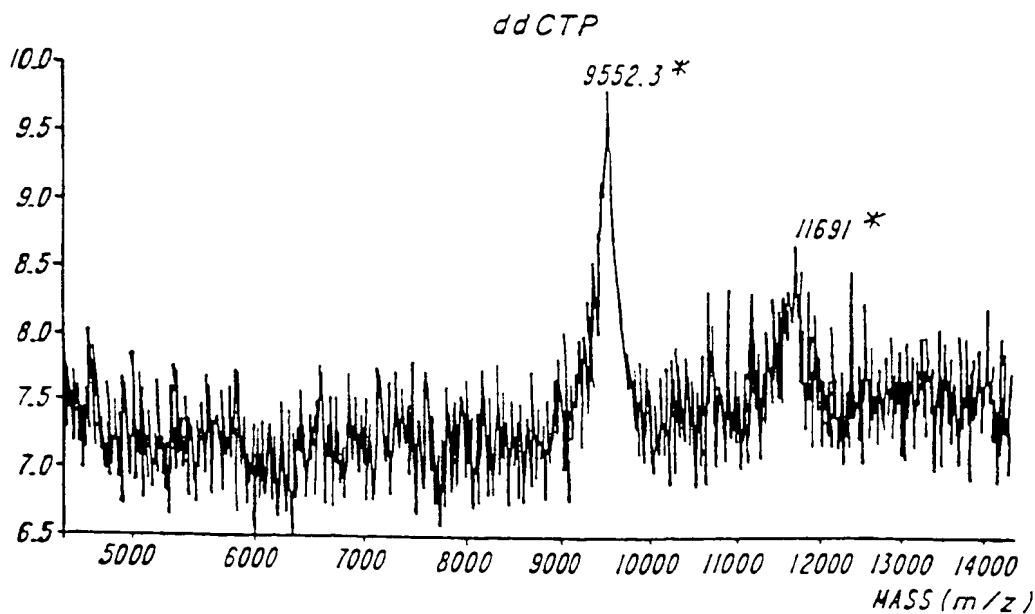
**FIG. 35A****FIG. 35B**

SUBSTITUTE SHEET (RULE 26)

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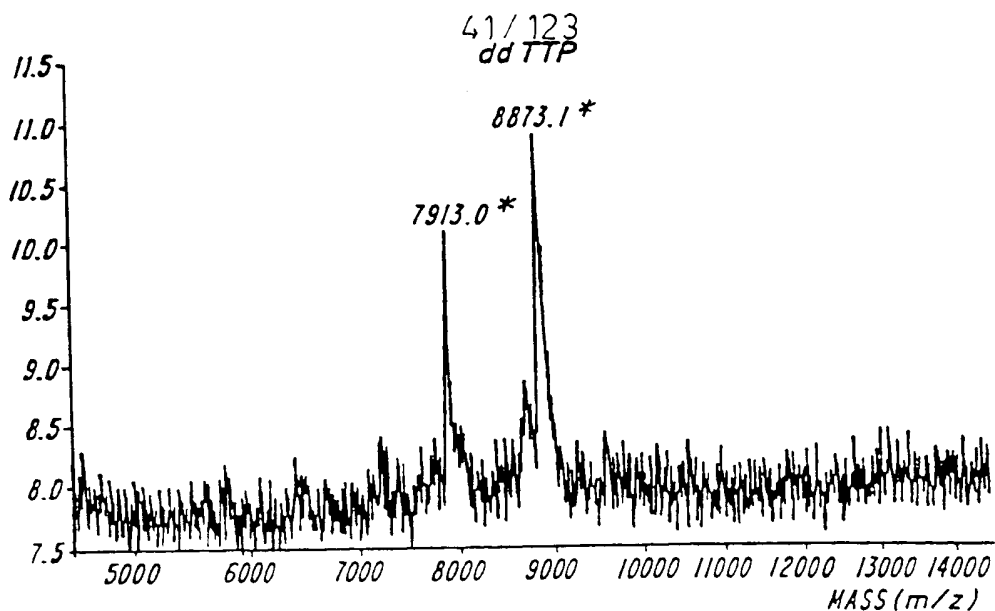


WILDTYPE (8908, 6 / 8846, 8)

FIG. 35C

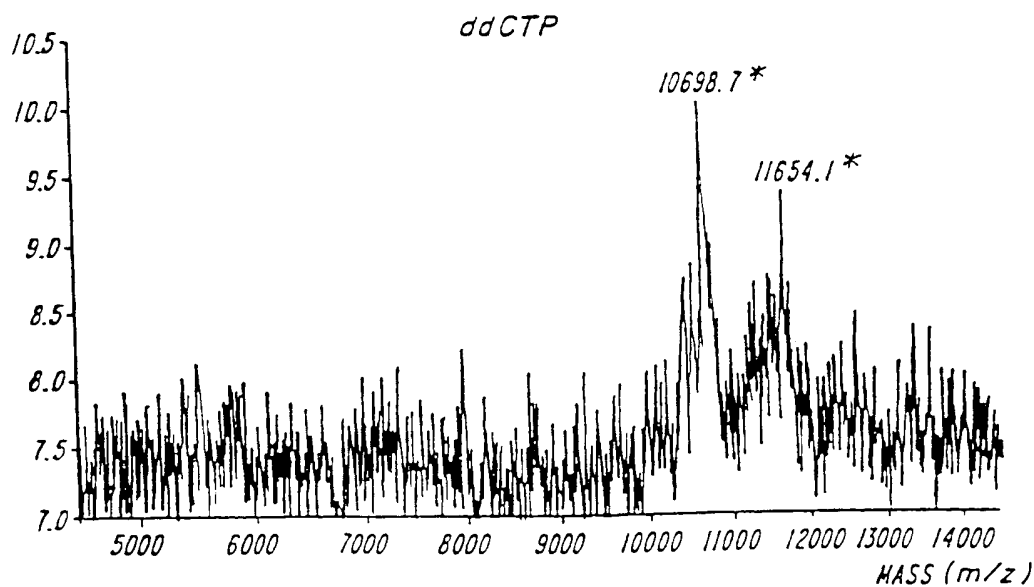
506S (9552, 3 / 9465, 2)
WILDTYPE (11691, 9 / 11612, 6)

FIG. 35D



$\Delta F508$ (7913,0/7891,2)
WILDTYPE (8873,1/8846,8)

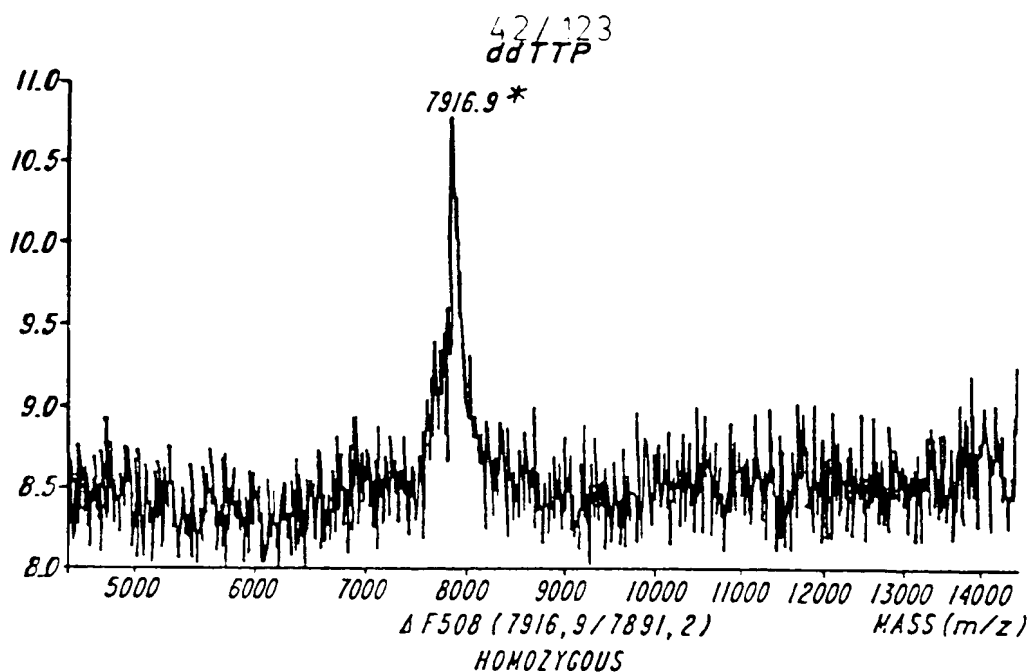
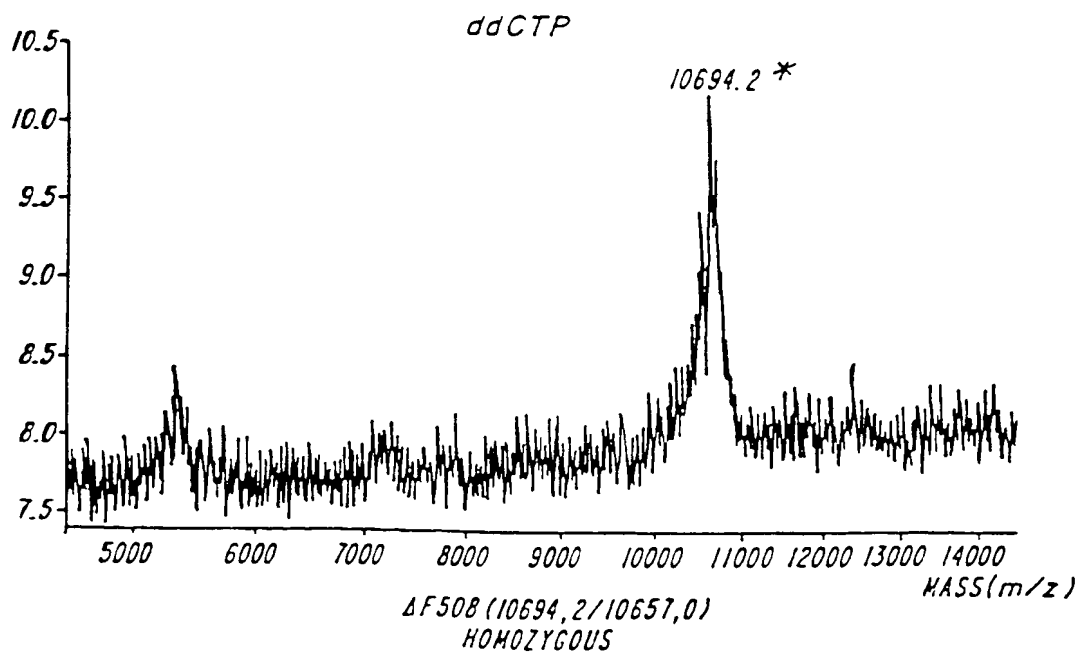
FIG. 35E



$\Delta 508$ (10698,7/10657,0)
WILDTYPE (11654,1/11612,6)

FIG. 35F

SUBSTITUTE SHEET (RULE 26)

**FIG. 35G****FIG. 35H**

SUBSTITUTE SHEET (RULE 26)

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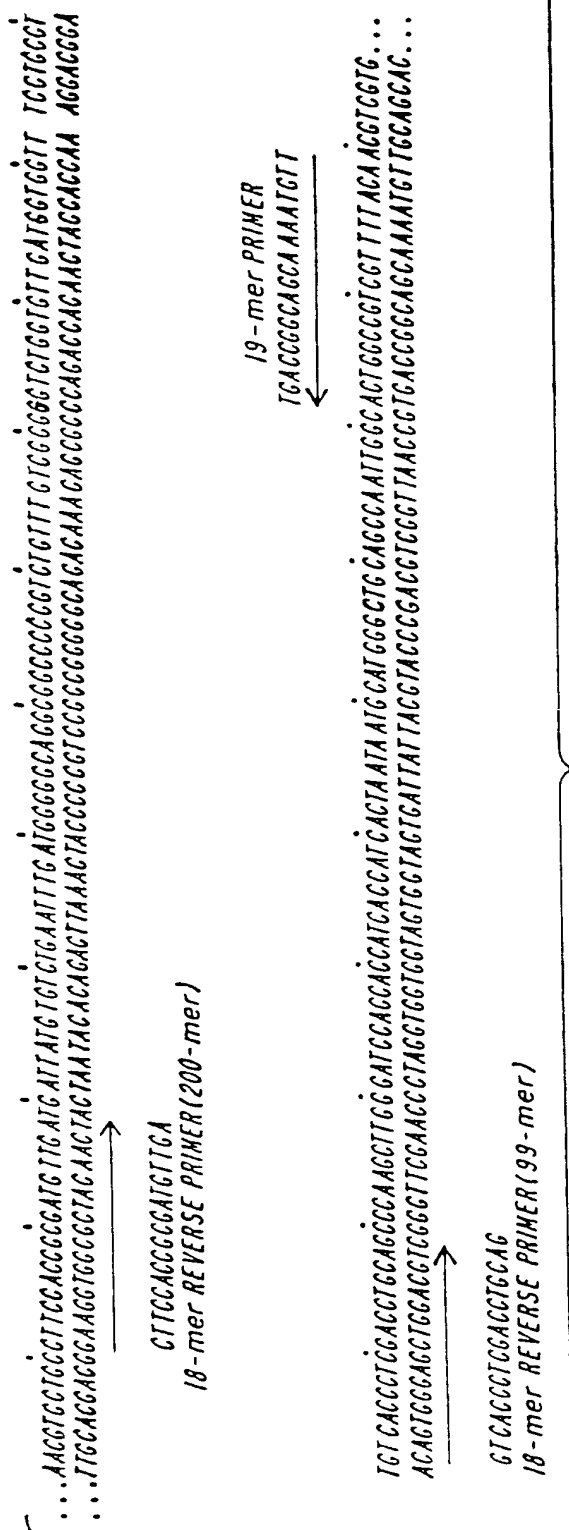


FIG. 36

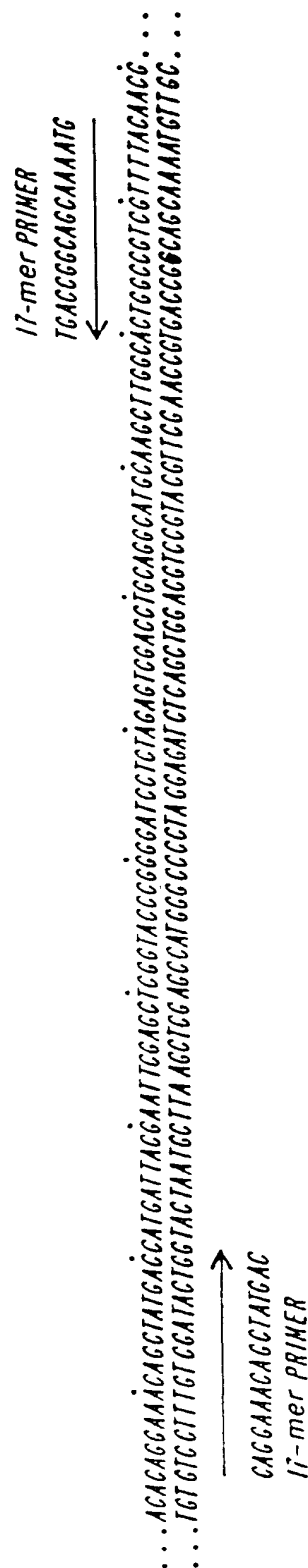
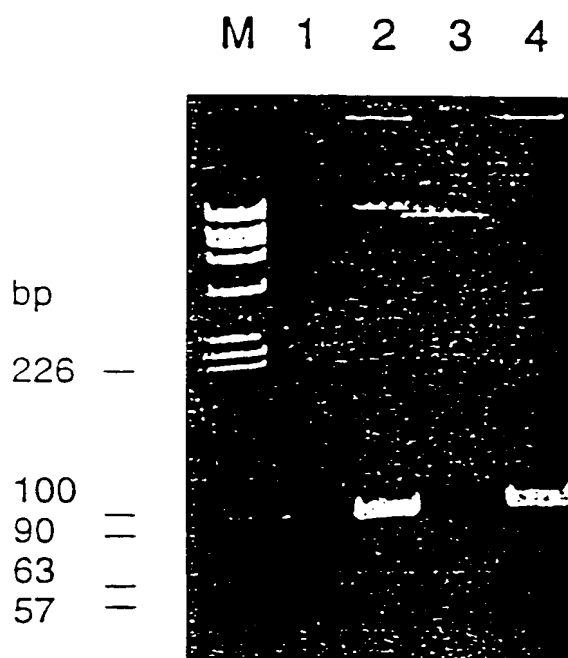


FIG. 37

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*FIG. 38*

1 2 3 4 5 6

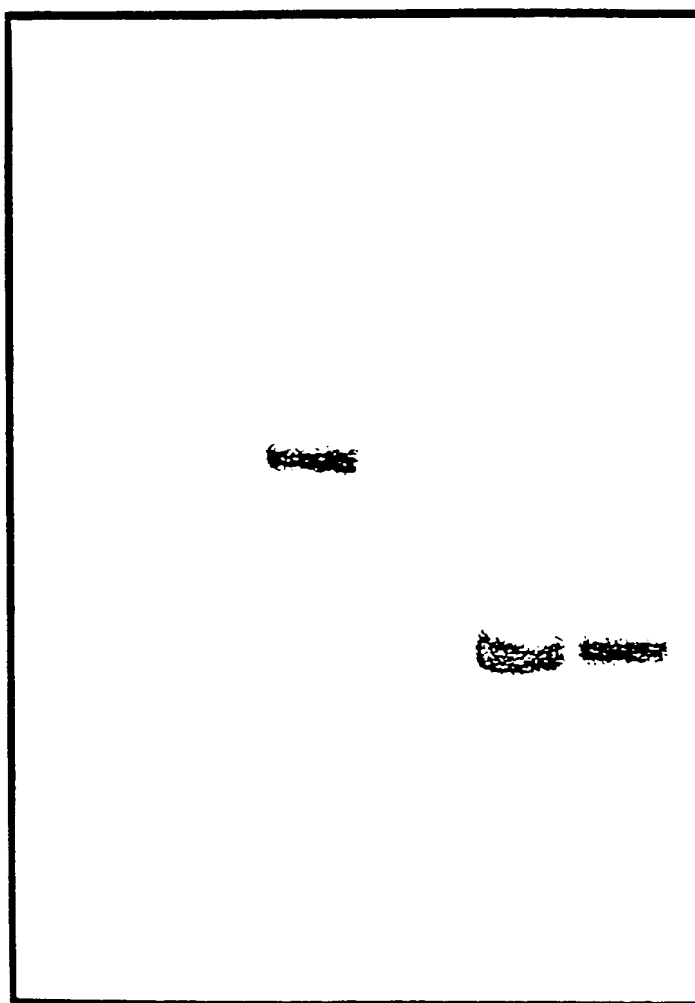


FIG. 39

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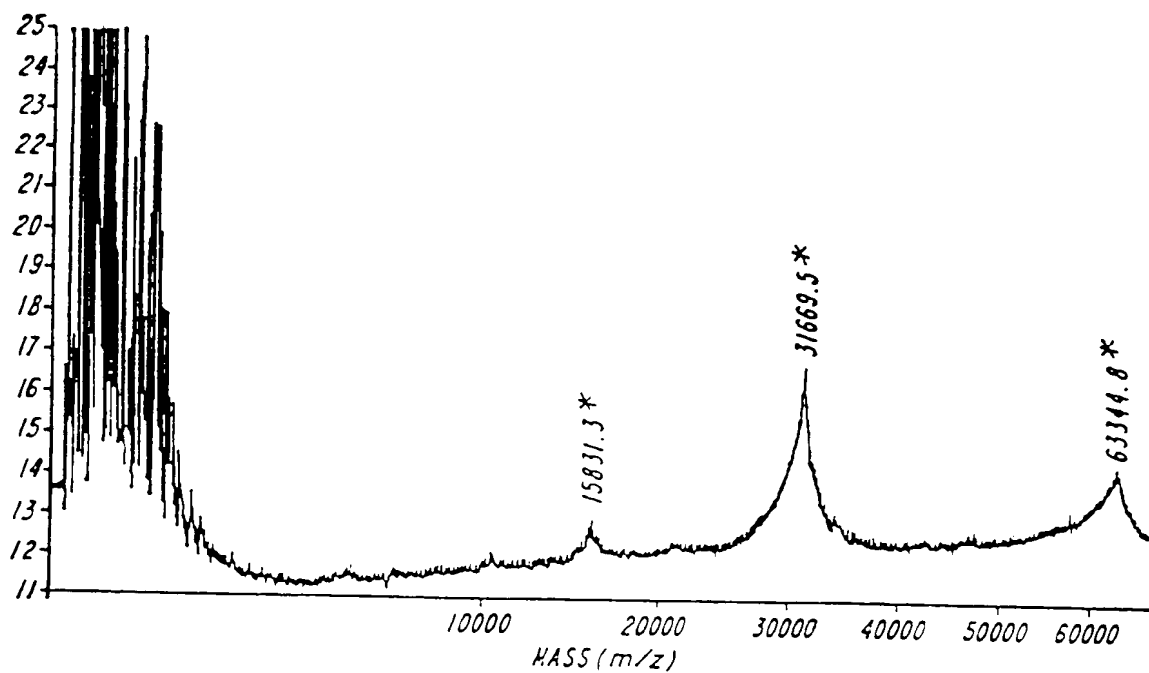


FIG. 40A

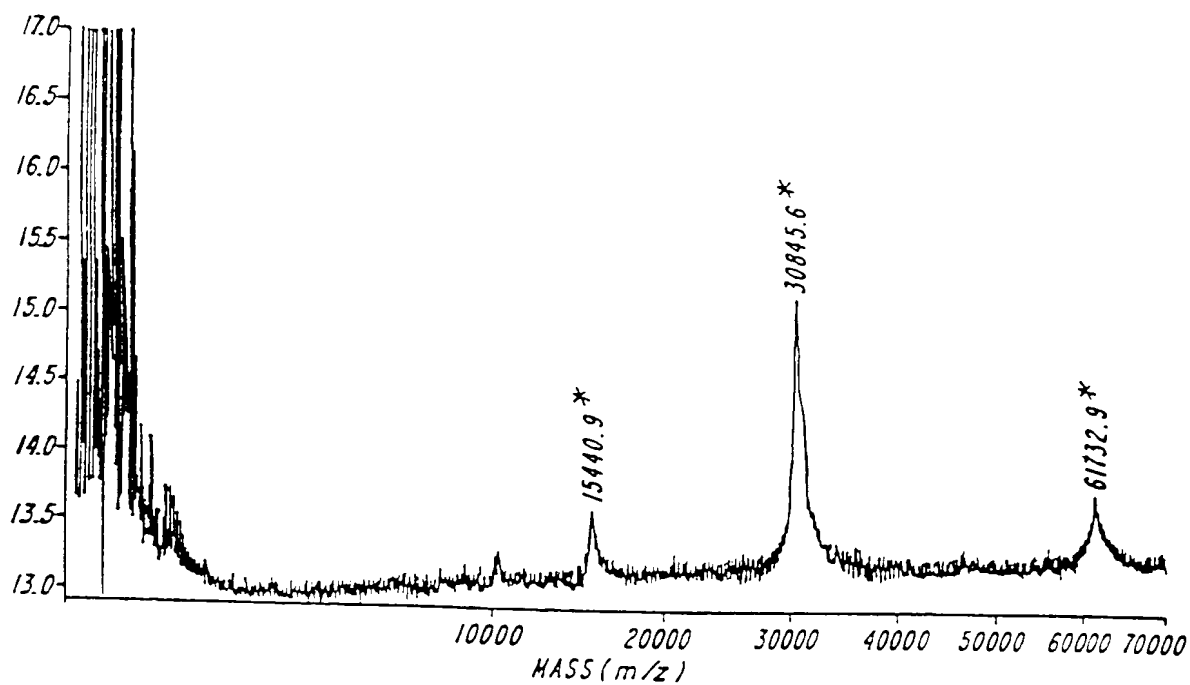
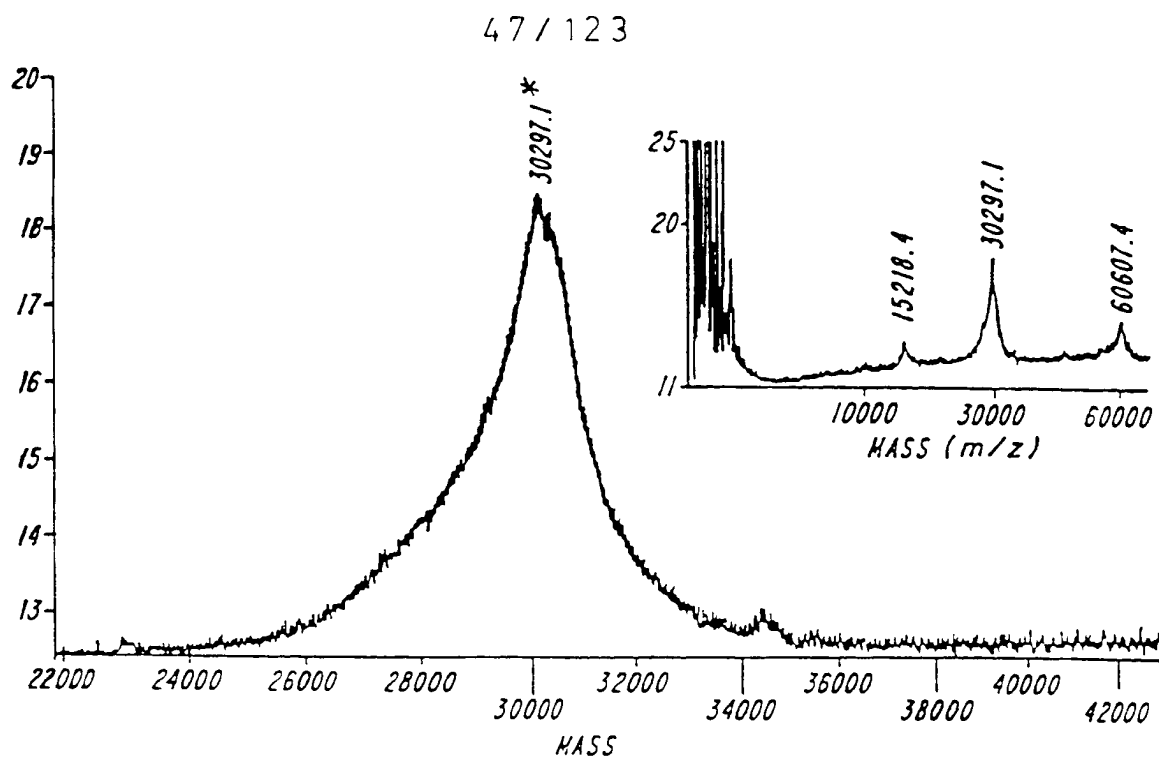
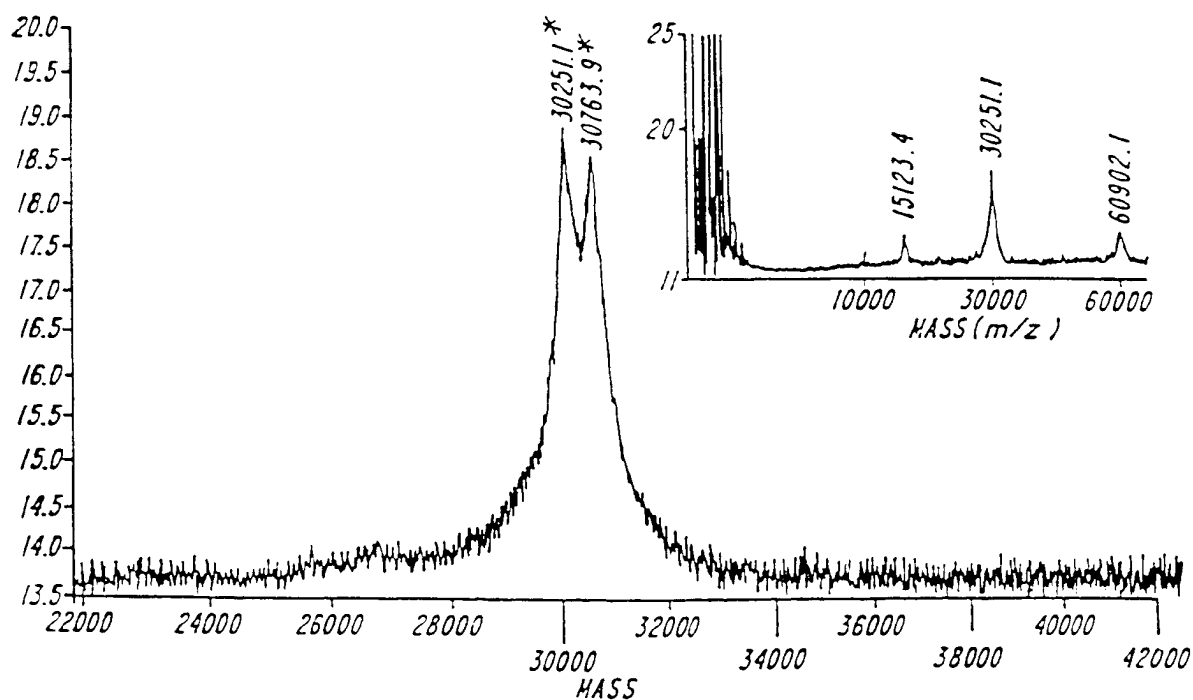


FIG. 40B

SUBSTITUTE SHEET (RULE 26)

**FIG. 41A****FIG. 41B**

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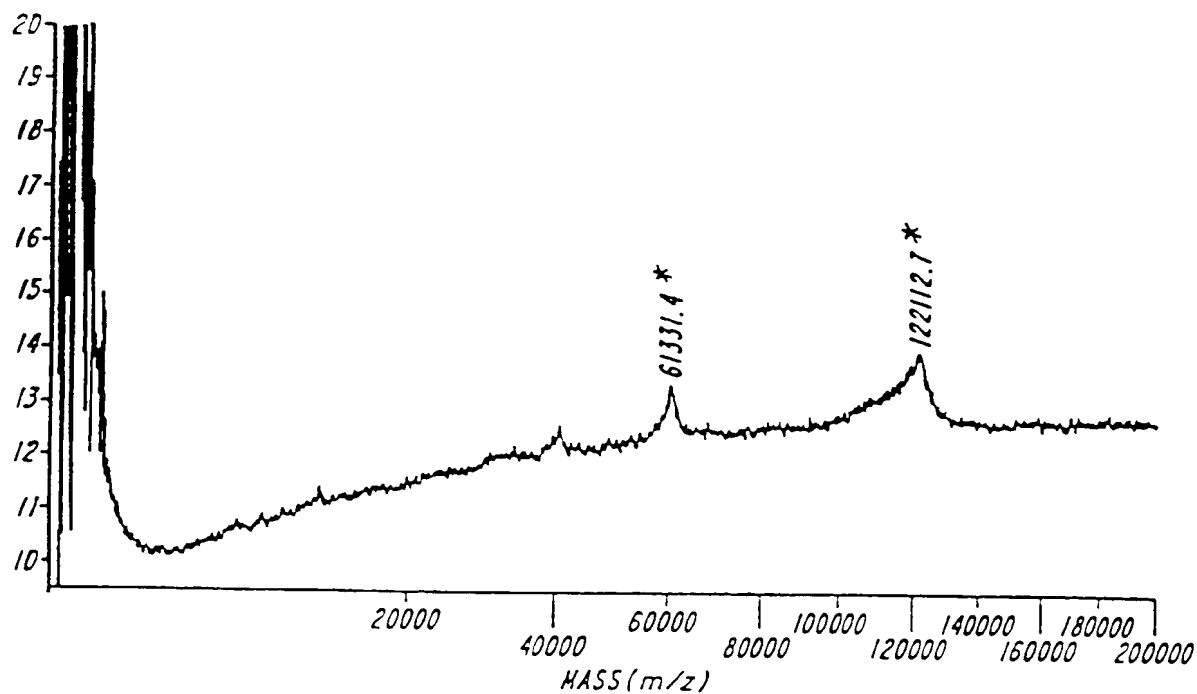


FIG. 42A

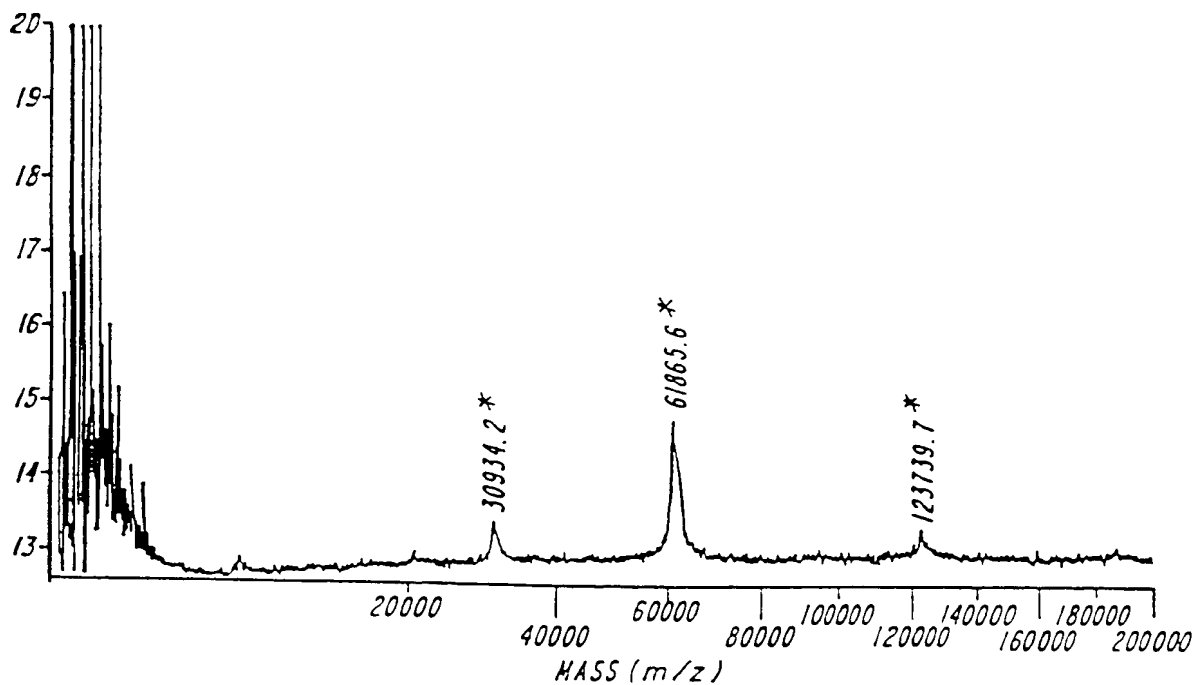


FIG. 42B

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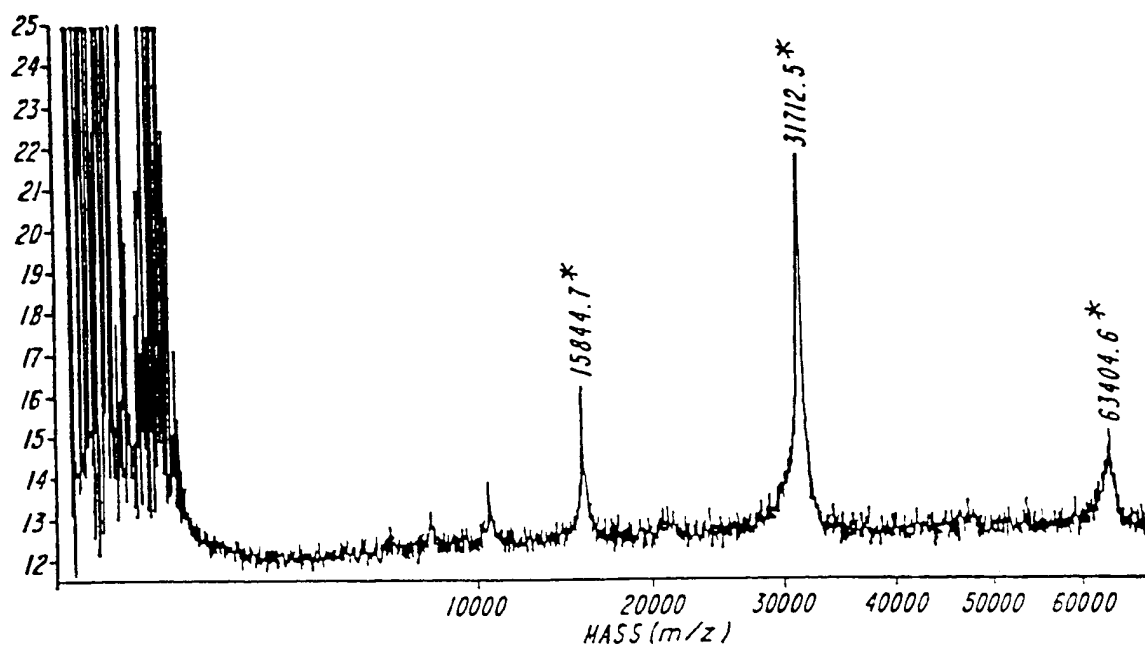


FIG. 43A

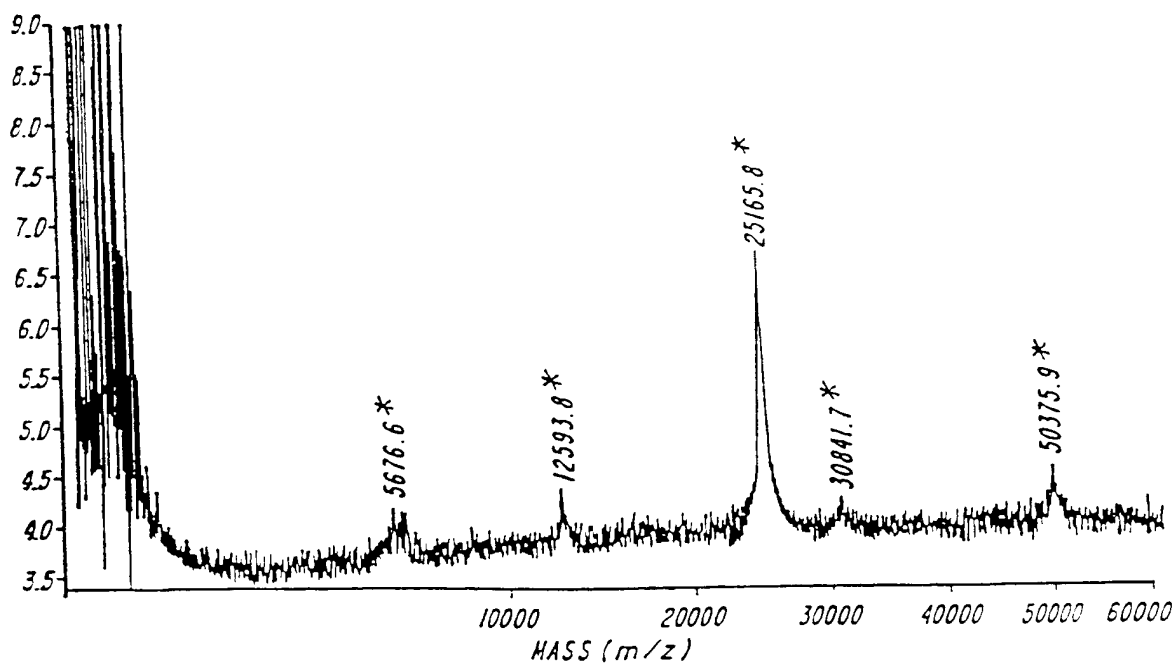


FIG. 43B

SUBSTITUTE SHEET (RULE 26)

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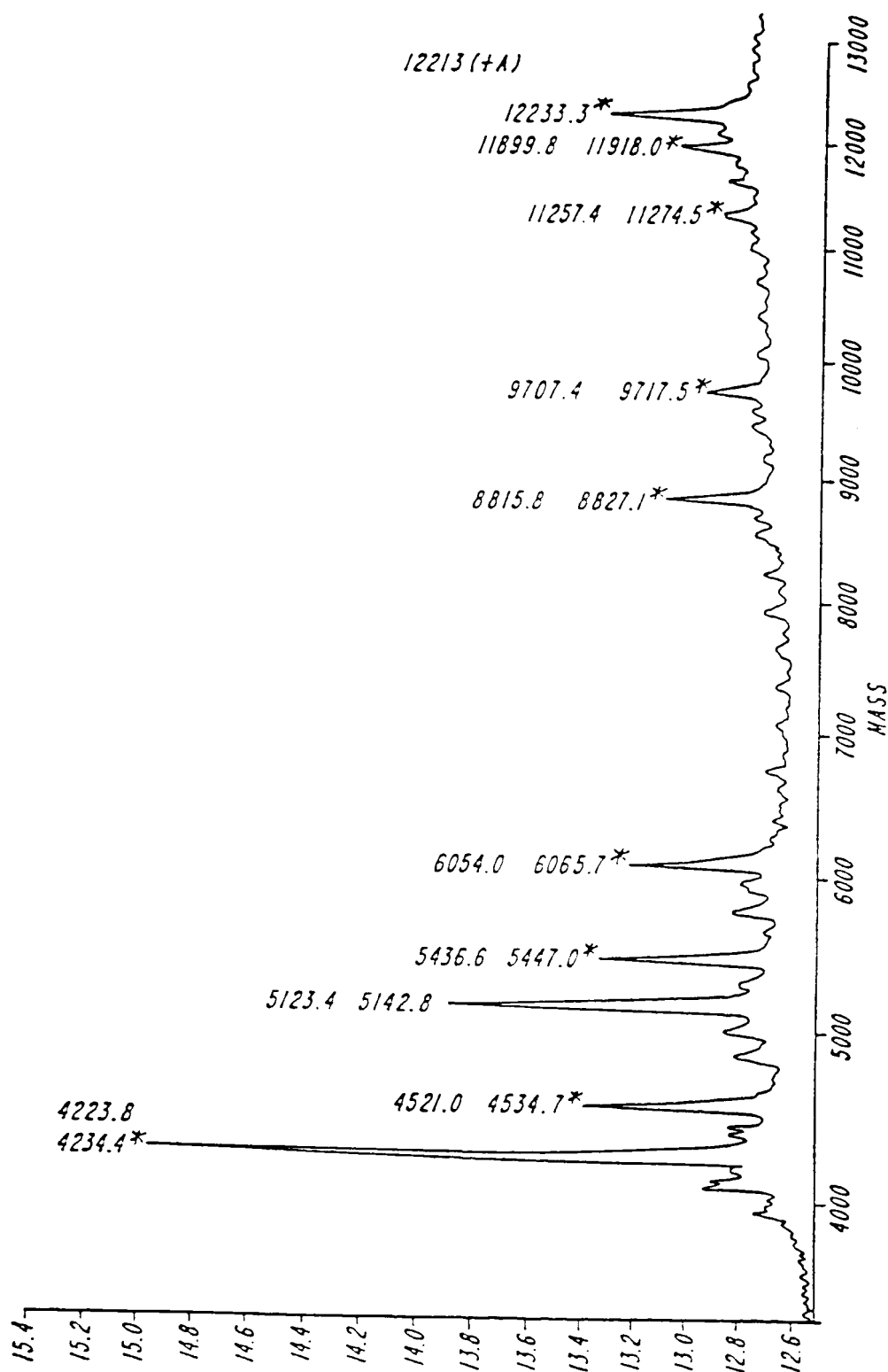


FIG. 44A

SUBSTITUTE SHEET (RULE 26)

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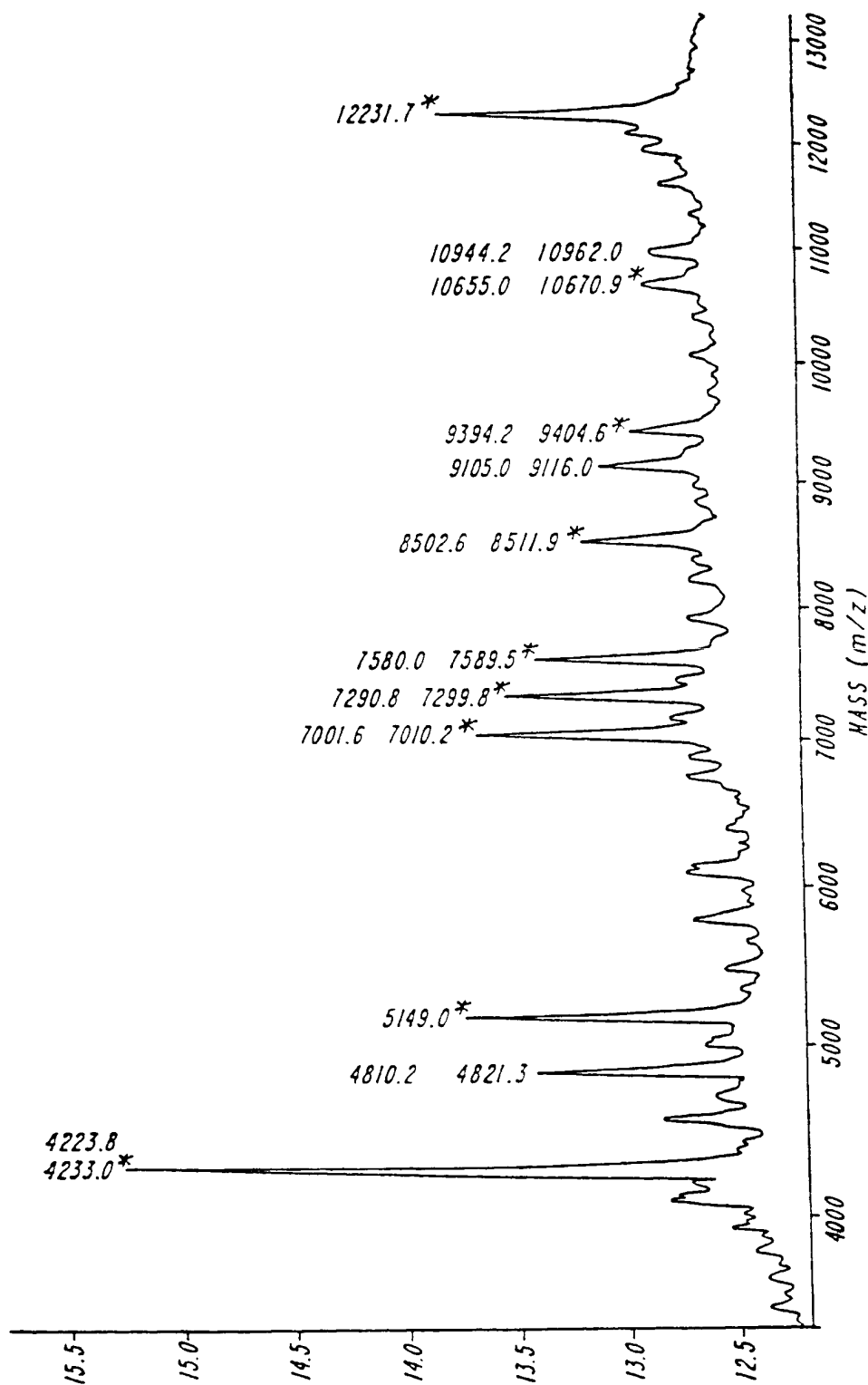


FIG. 44B

SUBSTITUTE SHEET (RULE 26)

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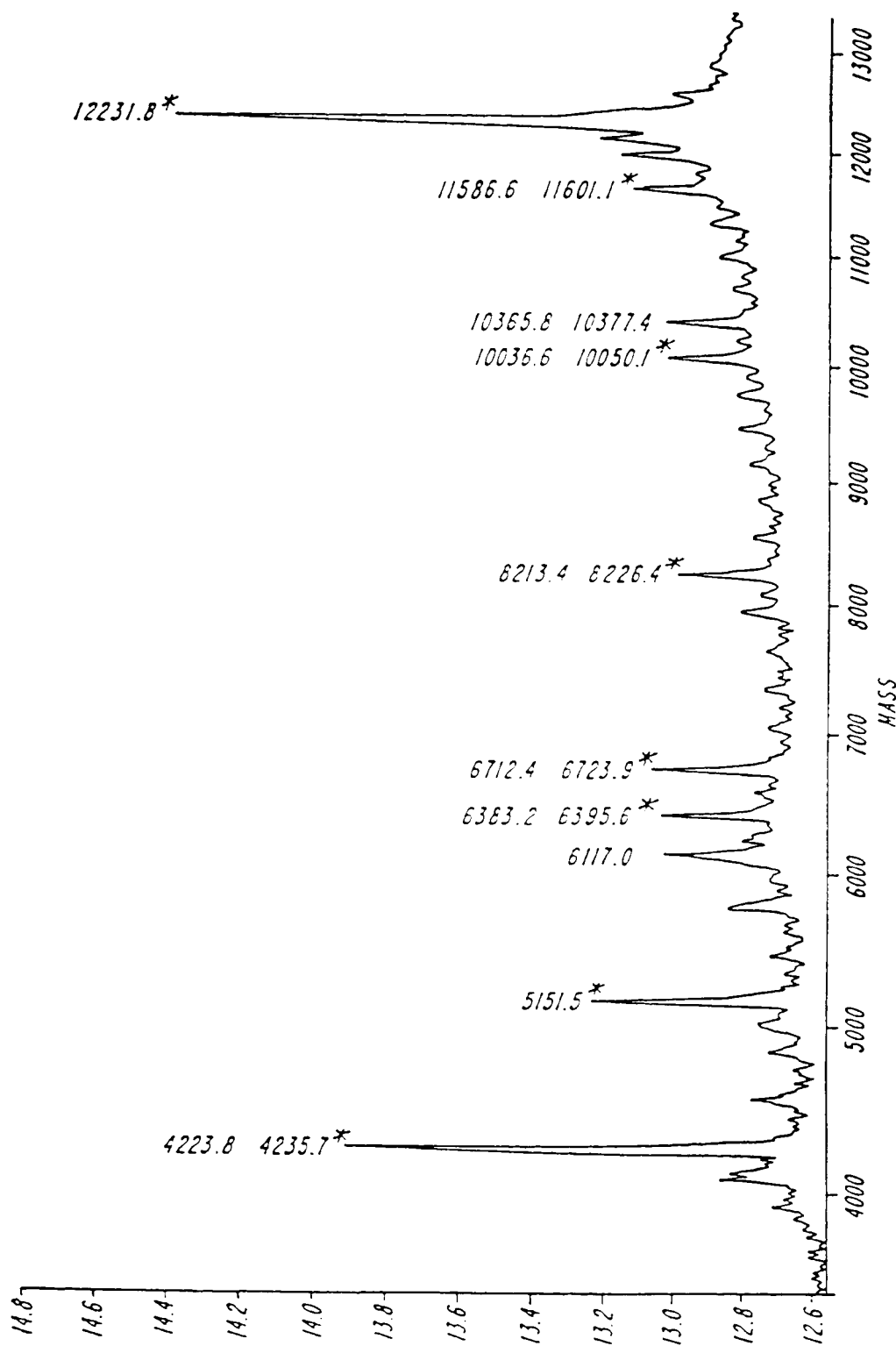


FIG. 44C

SUBSTITUTE SHEET (RULE 26)

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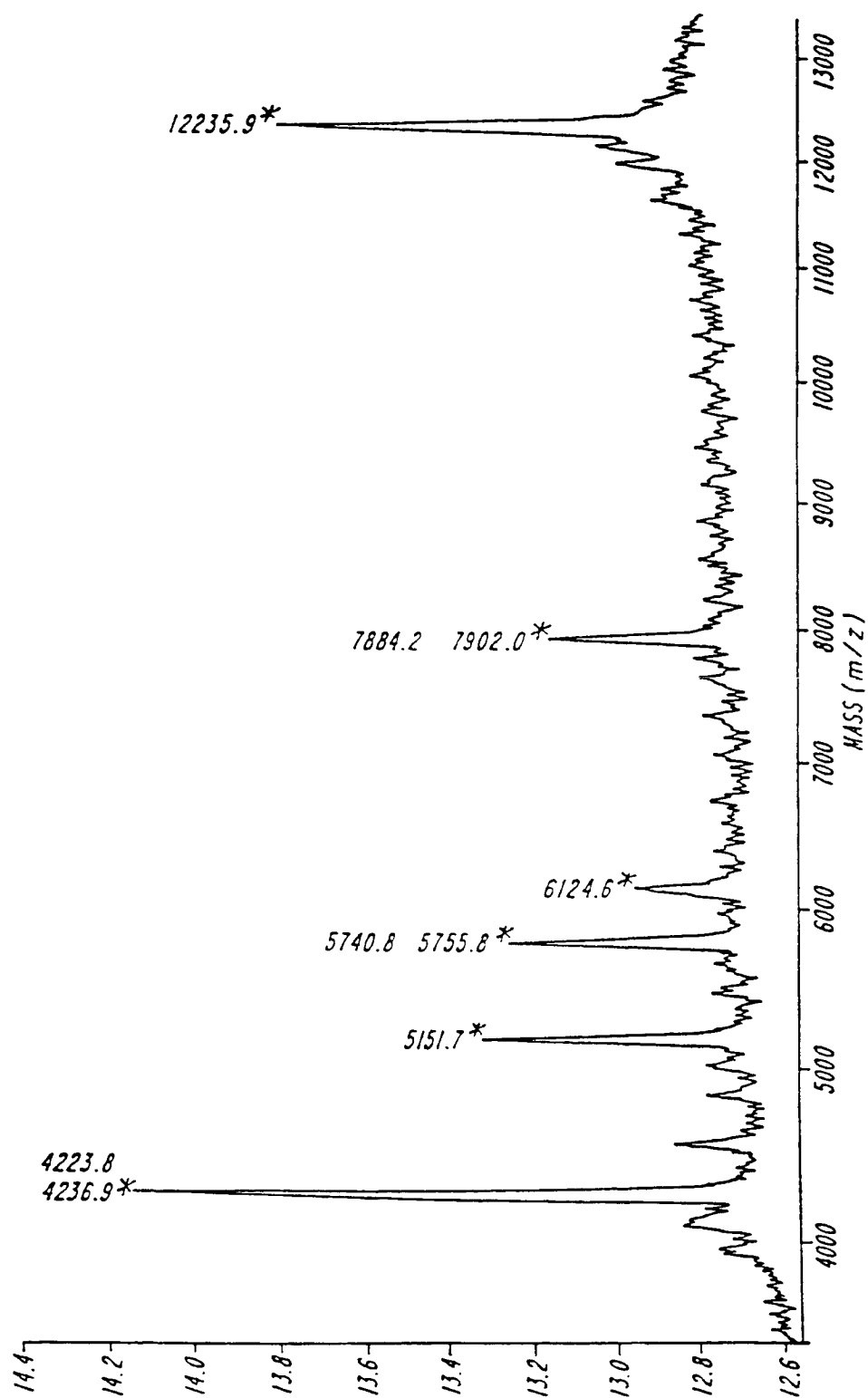


FIG. 44D

SUBSTITUTE SHEET (RULE 26)

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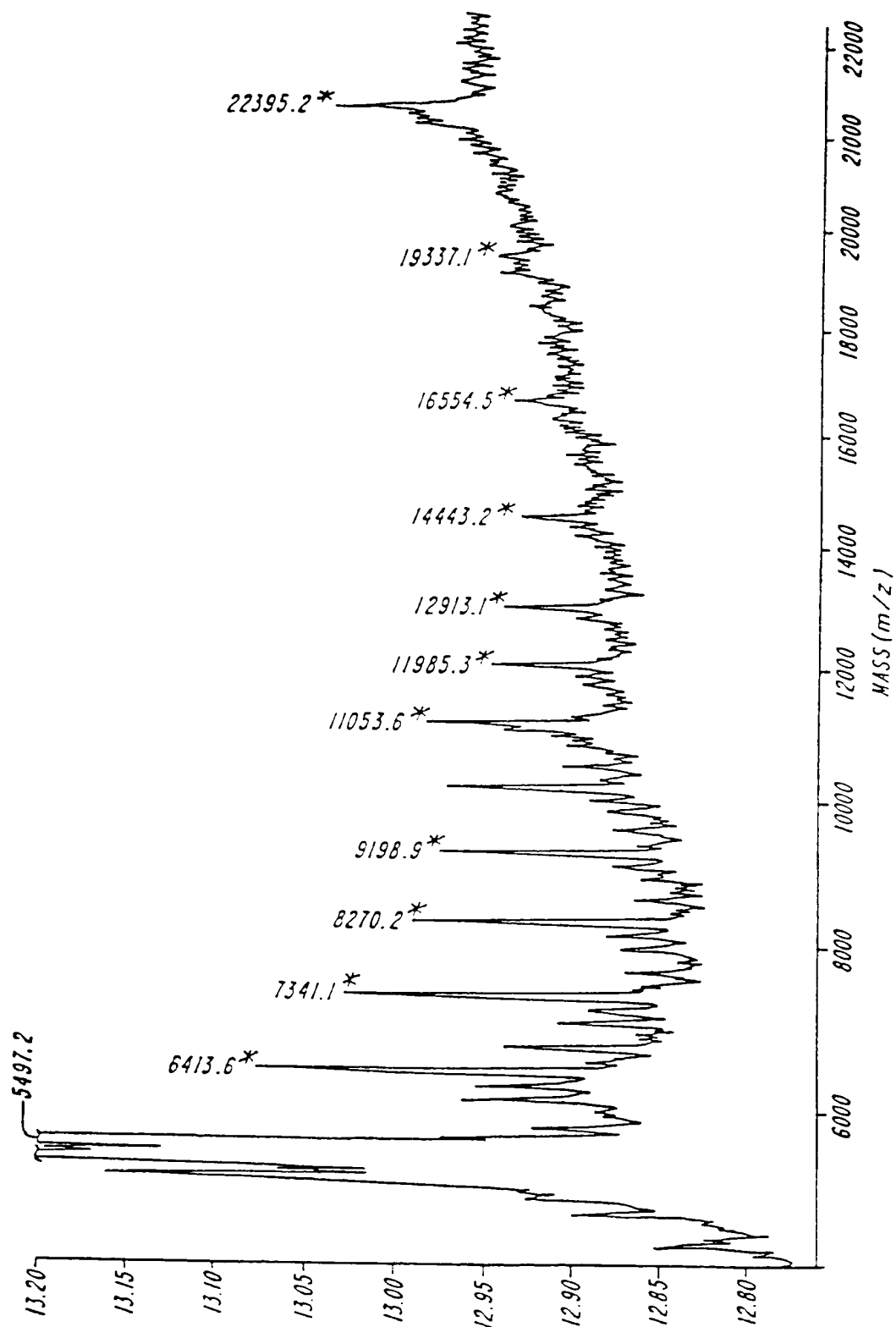
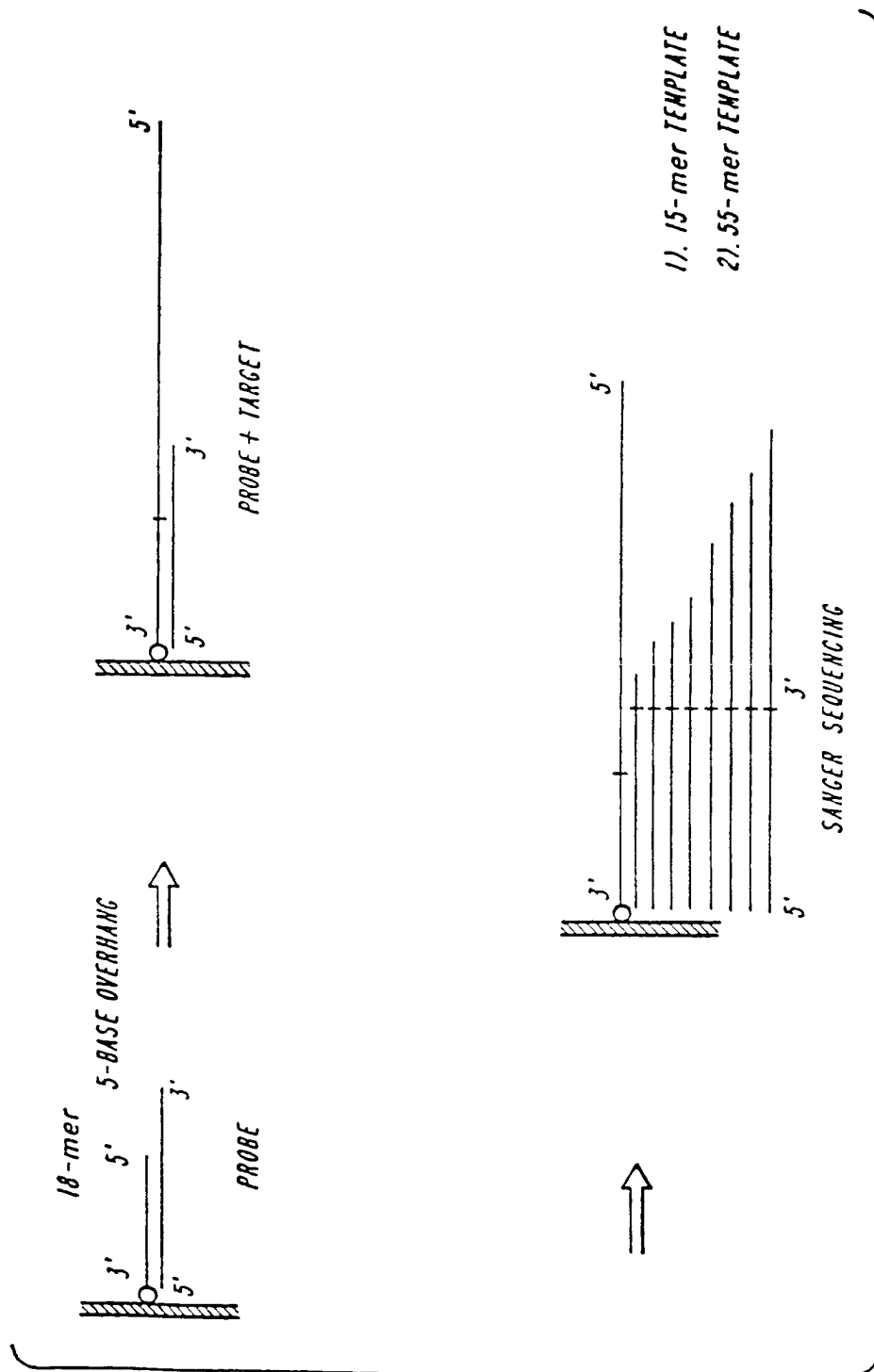


FIG. 45

SUBSTITUTE SHEET (RULE 26)



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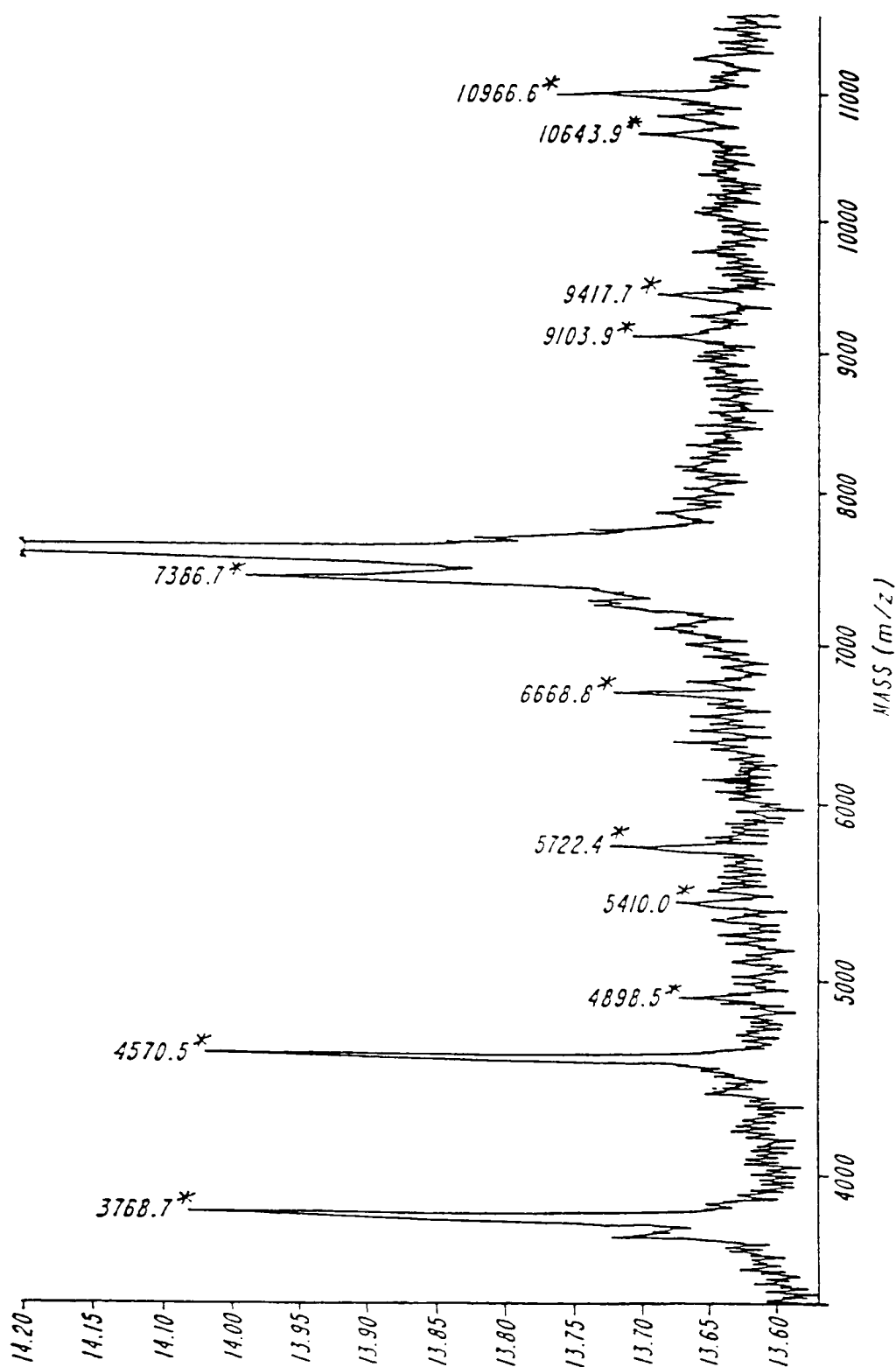


FIG. 47A

SUBSTITUTE SHEET (RULE 26)

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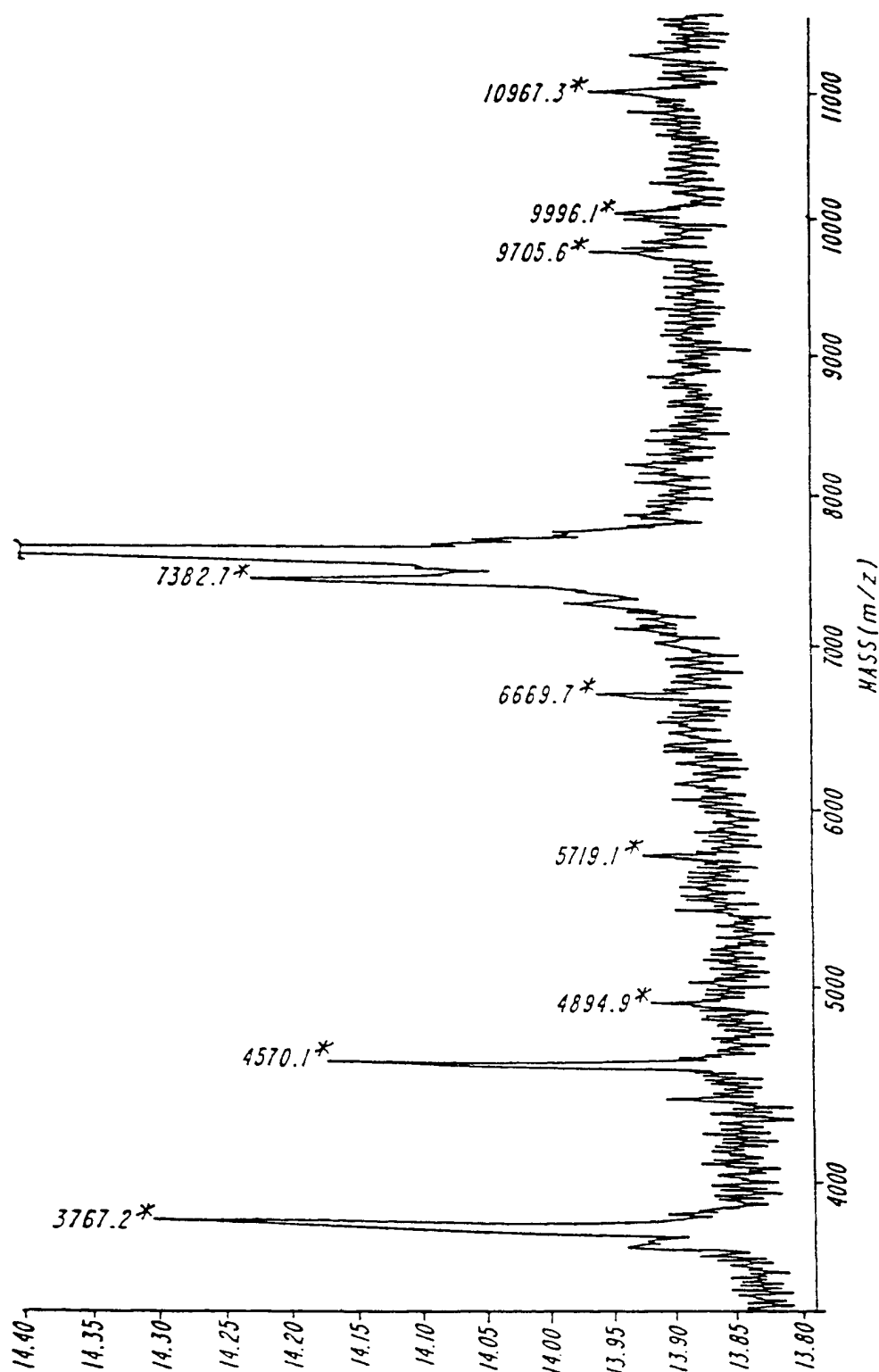


FIG. 47B

SUBSTITUTE SHEET (RULE 26)

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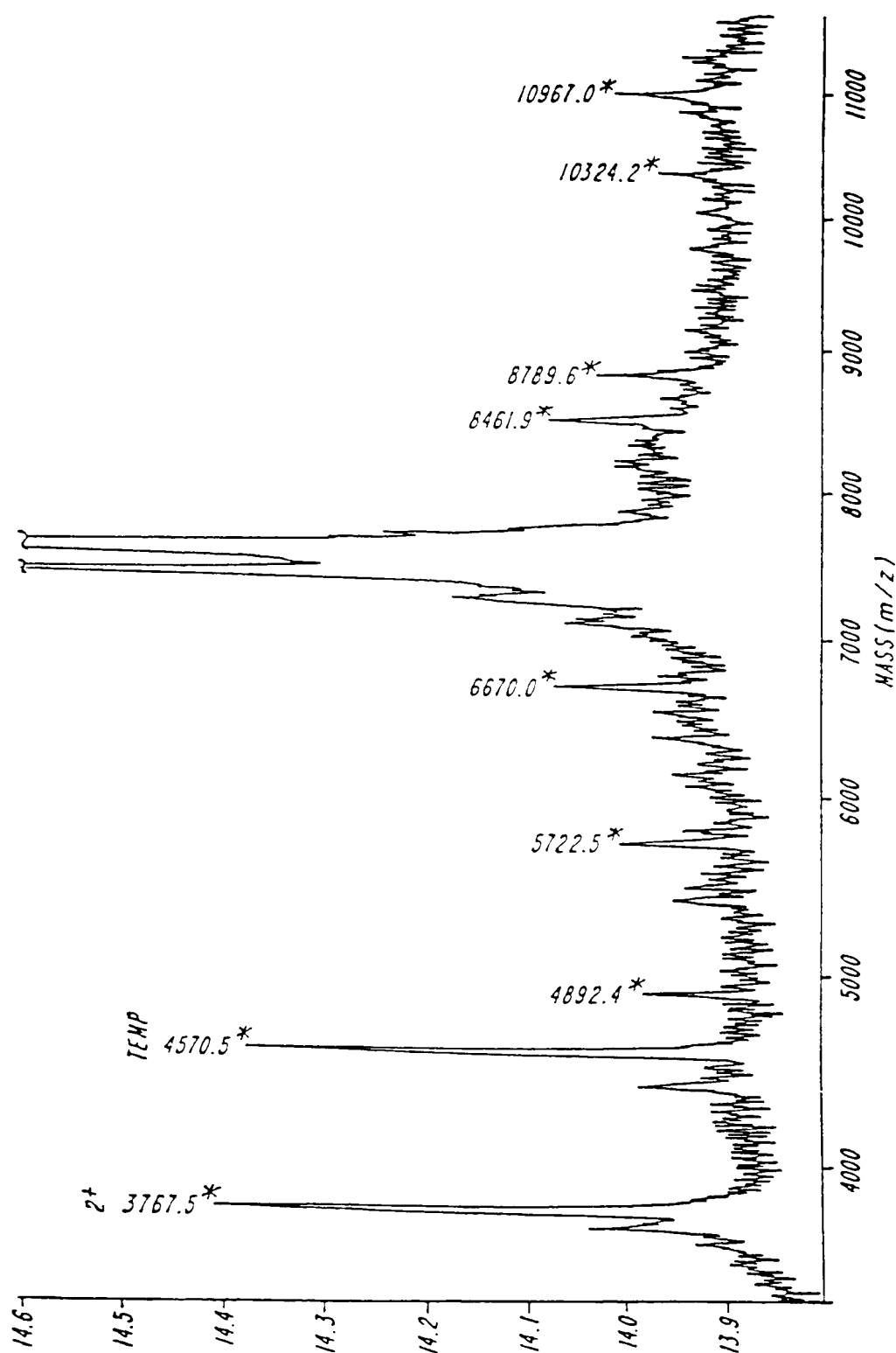


FIG. 47C

SUBSTITUTE SHEET (RULE 26)

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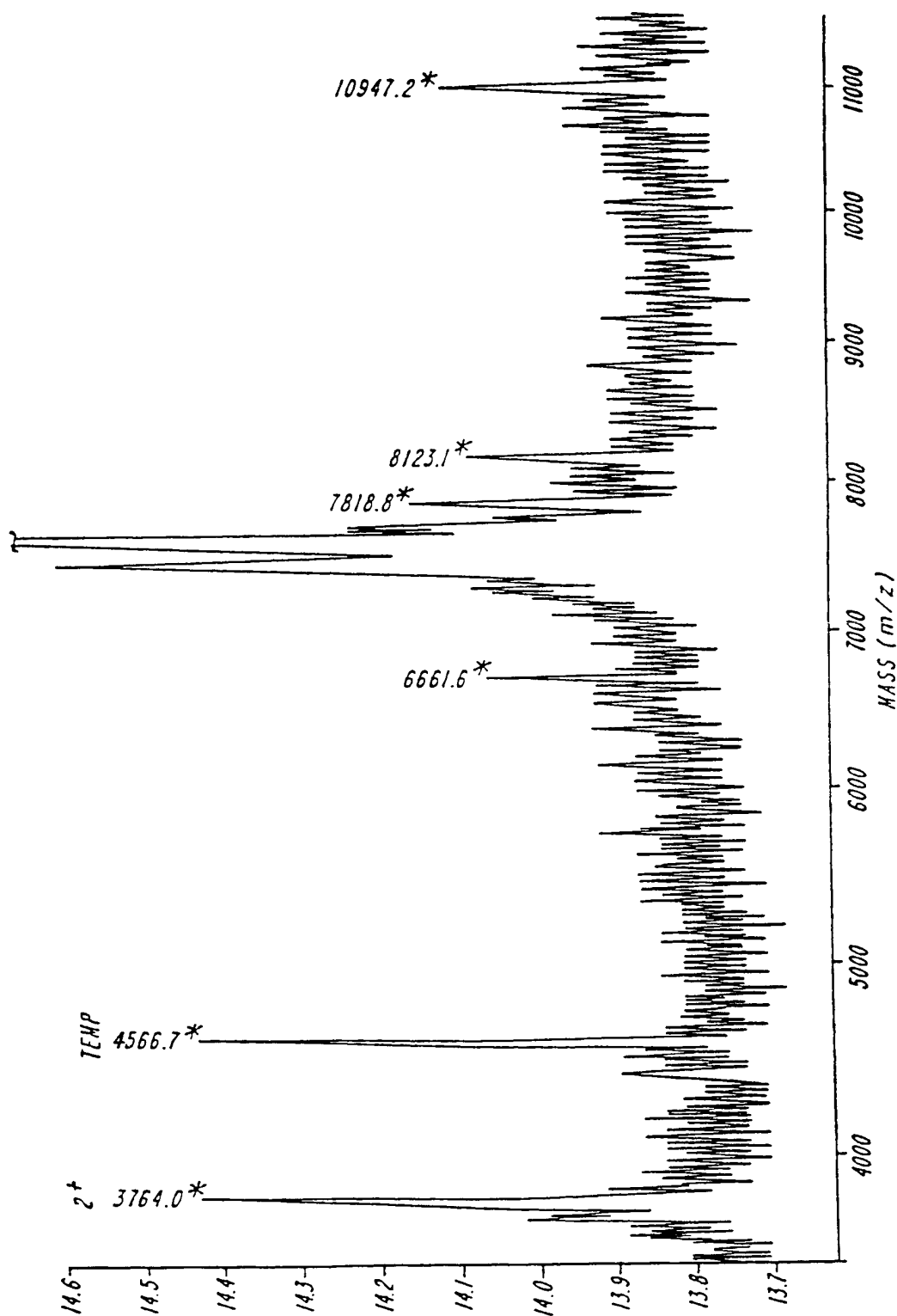
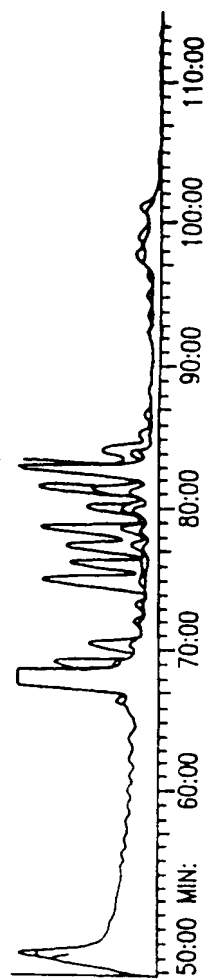
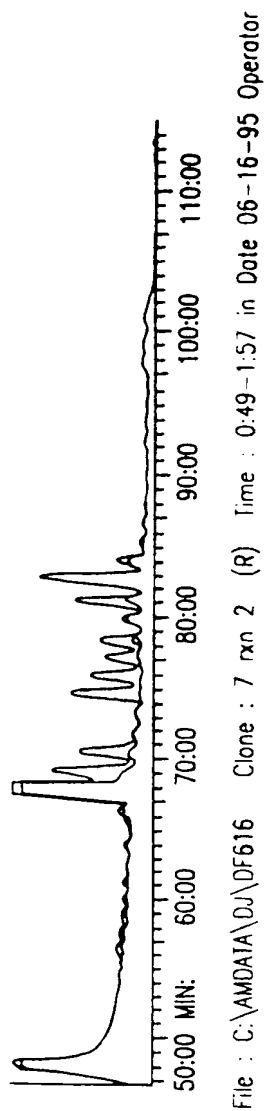
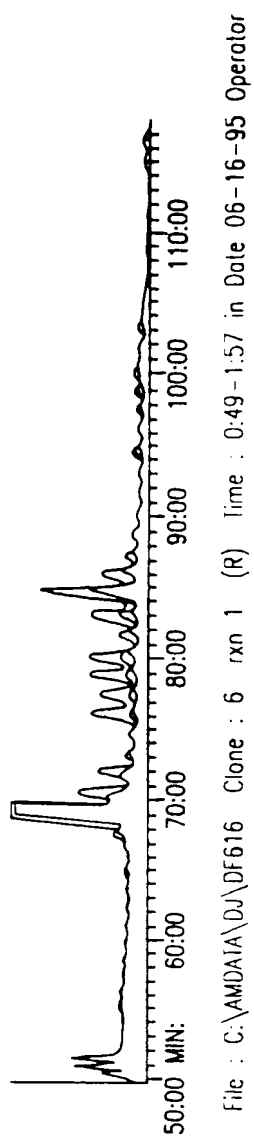
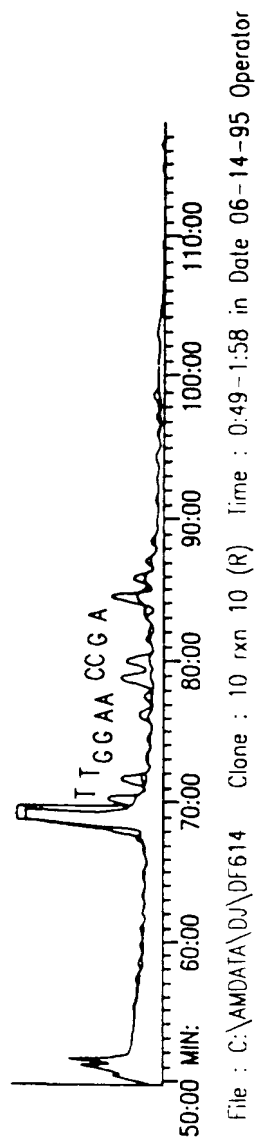


FIG. 47D

SUBSTITUTE SHEET (RULE 26)

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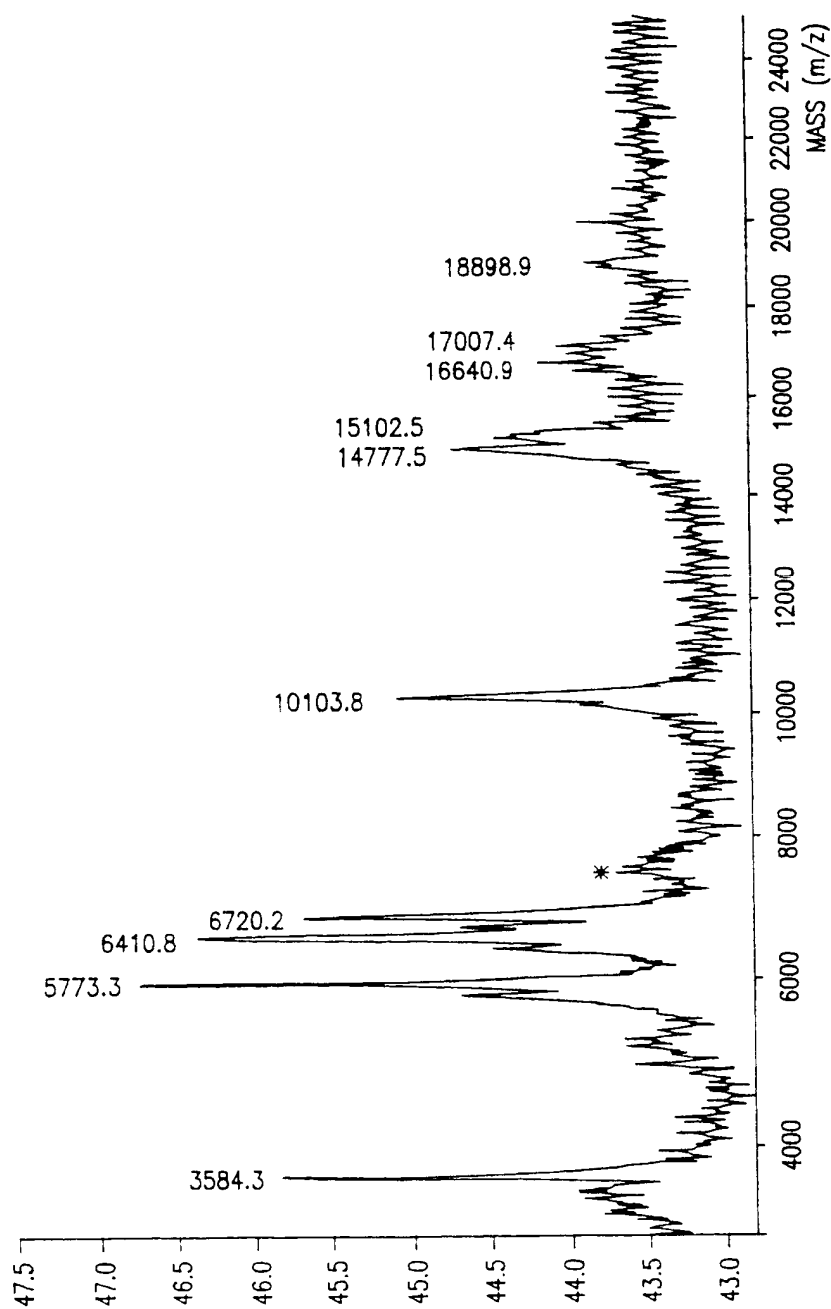


FIG. 49A

SUBSTITUTE SHEET (RULE 26)

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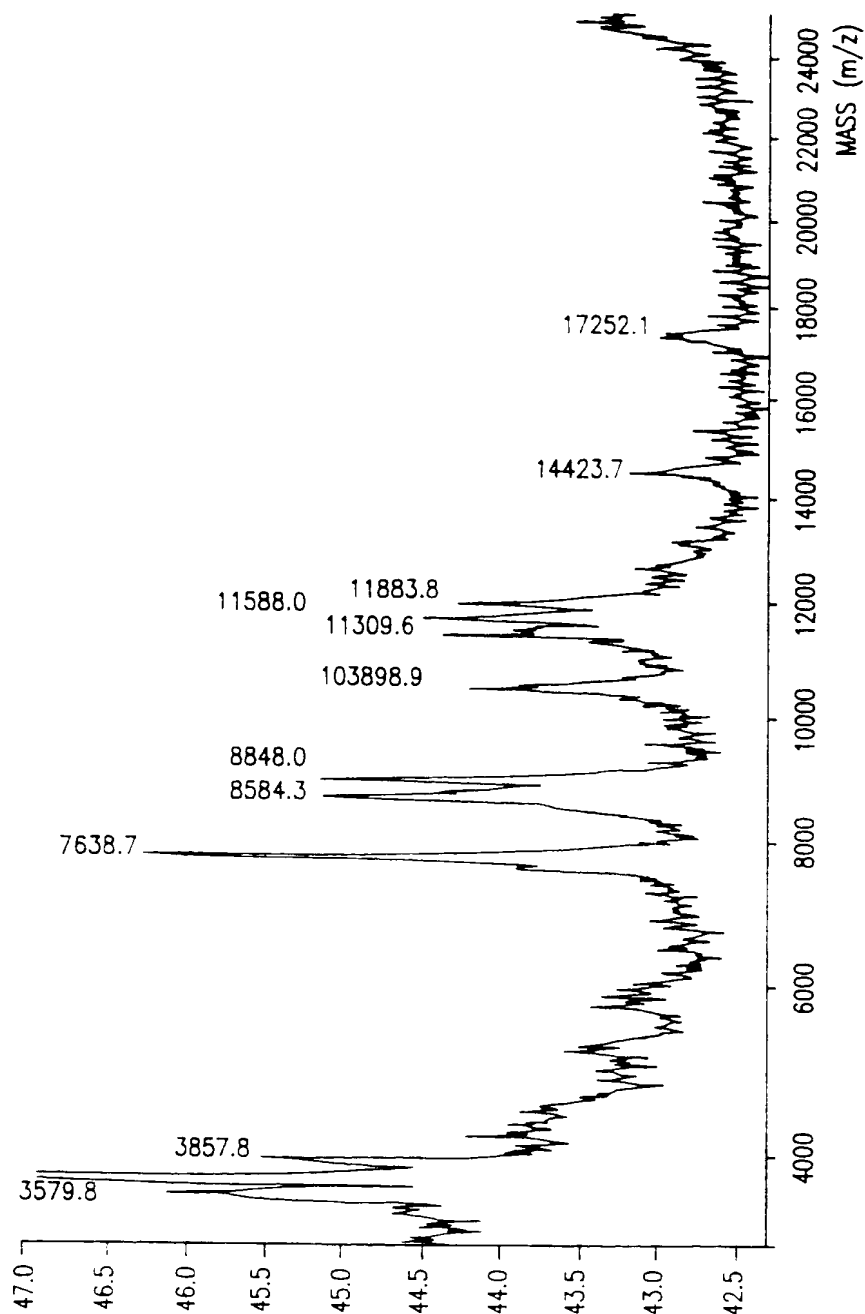


FIG. 49B

SUBSTITUTE SHEET (RULE 26)

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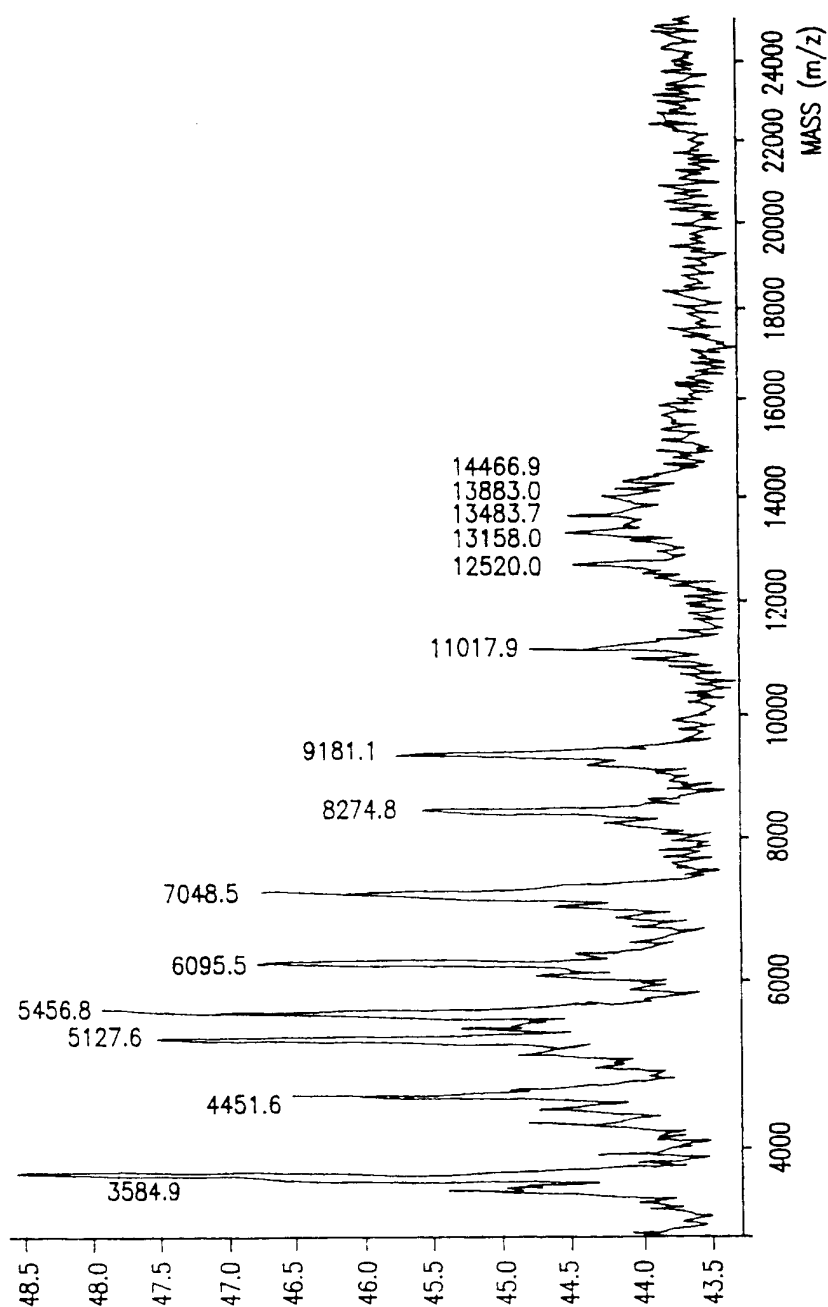


FIG. 49C

SUBSTITUTE SHEET (RULE 26)

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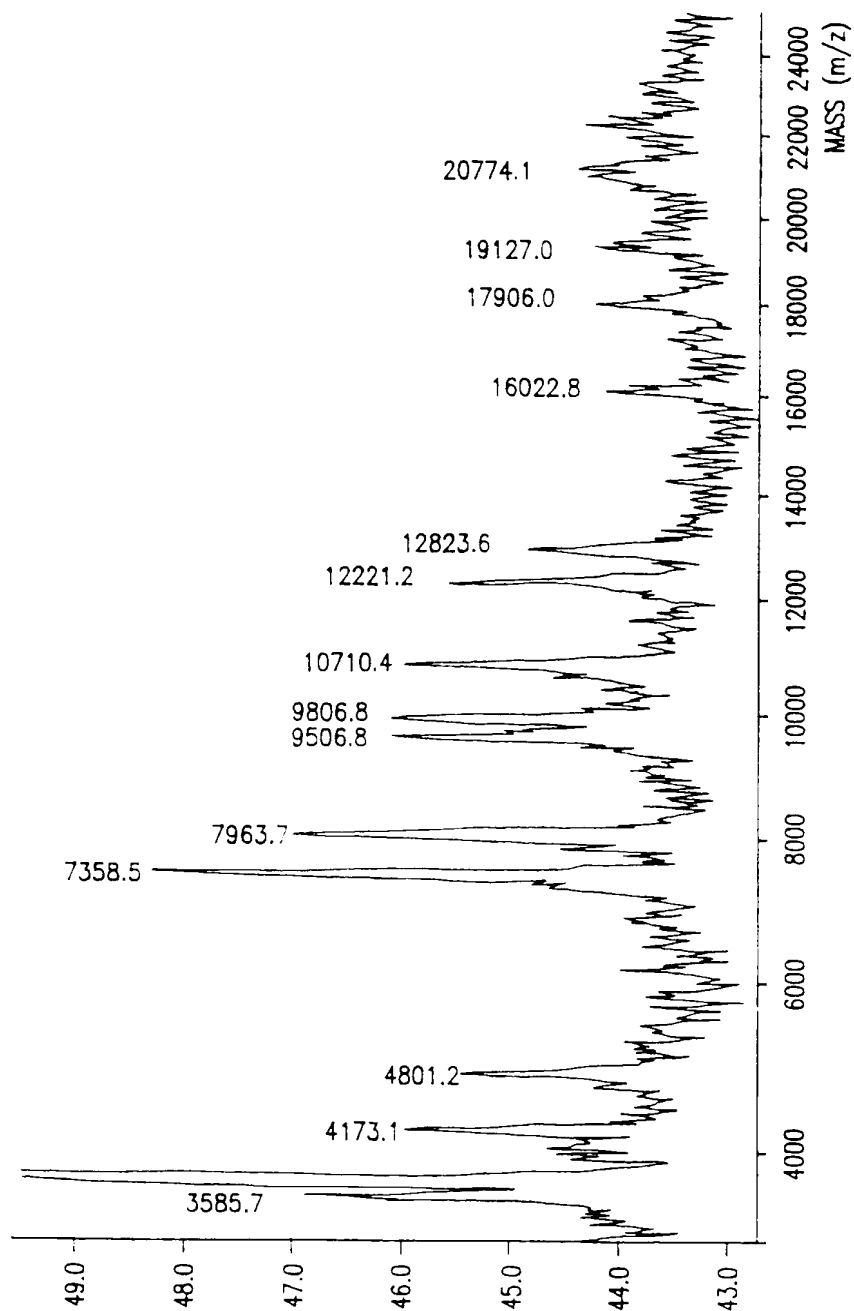


FIG. 49D

SUBSTITUTE SHEET (RULE 26)

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PARTIAL SEQUENCE OF THE β -GLOBIN TEMPLATE
 3'-(H)_n-ACCACGTGGACTGAG GACACCTCTT CAGACGGCAA TGACGOGACA CCCC GTTCCA CTGACACCTA-(N)_n-5'

5-TGCACCTGACTC	3' (PRIME)
5-TGCACCTGACTC	C-3'
5-TGCACCTGACTC	CT-3'
5-TGCACCTGACTC	CTG-3'
5-TGCACCTGACTC	CTGT-3'
5-TGCACCTGACTC	CTGTG-3'
5-TGCACCTGACTC	CTGTGG-3'
5-TGCACCTGACTC	CTGTGGA-3'
5-TGCACCTGACTC	CTGTGGAG-3'
5-TGCACCTGACTC	CTGTGGAGA-3'
5-TGCACCTGACTC	CTGTGGAGAA-3'
5-TGCACCTGACTC	CTGTGGAGAA G-3'
5-TGCACCTGACTC	CTGTGGAGAA GT-3'
5-TGCACCTGACTC	CTGTGGAGAA GTC-3'
5-TGCACCTGACTC	CTGTGGAGAA GTCT-3'
5-TGCACCTGACTC	CTGTGGAGAA GTCTG-3'
5-TGCACCTGACTC	CTGTGGAGAA GTCTGC-3'
5-TGCACCTGACTC	CTGTGGAGAA GTCTGCC-3'
5-TGCACCTGACTC	CTGTGGAGAA GTCTGCCG-3'
5-TGCACCTGACTC	CTGTGGAGAA GTCTGCCGT-3'
5-TGCACCTGACTC	CTGTGGAGAA GTCTGCCGTT-3'
5-TGCACCTGACTC	CTGTGGAGAA GTCTGCCGTT A-3'
5-TGCACCTGACTC	CTGTGGAGAA GTCTGCCGTT AC-3'
5-TGCACCTGACTC	CTGTGGAGAA GTCTGCCGTT ACT-3'
5-TGCACCTGACTC	CTGTGGAGAA GTCTGCCGTT ACTG-3'
5-TGCACCTGACTC	CTGTGGAGAA GTCTGCCGTT ACTGC-3'
5-TGCACCTGACTC	CTGTGGAGAA GTCTGCCGTT ACTGCC-3'
5-TGCACCTGACTC	CTGTGGAGAA GTCTGCCGTT ACTGCC-3'
5-TGCACCTGACTC	CTGTGGAGAA GTCTGCCGTT ACTGCCCT-3'
5-TGCACCTGACTC	CTGTGGAGAA GTCTGCCGTT ACTGCCCTG-3'
5-TGCACCTGACTC	CTGTGGAGAA GTCTGCCGTT ACTGCCCTGT-3'
5-TGCACCTGACTC	CTGTGGAGAA GTCTGCCGTT ACTGCCCTGT G-3'
5-TGCACCTGACTC	CTGTGGAGAA GTCTGCCGTT ACTGCCCTGT GG-3'
5-TGCACCTGACTC	CTGTGGAGAA GTCTGCCGTT ACTGCCCTGT GGG-3'
5-TGCACCTGACTC	CTGTGGAGAA GTCTGCCGTT ACTGCCCTGT GGGG-3'
5-TGCACCTGACTC	CTGTGGAGAA GTCTGCCGTT ACTGCCCTGT GGGGC-3'
5-TGCACCTGACTC	CTGTGGAGAA GTCTGCCGTT ACTGCCCTGT GGGGCA-3'
5-TGCACCTGACTC	CTGTGGAGAA GTCTGCCGTT ACTGCCCTGT GGGGCAA-3'
5-TGCACCTGACTC	CTGTGGAGAA GTCTGCCGTT ACTGCCCTGT GGGGCAAG-3'
5-TGCACCTGACTC	CTGTGGAGAA GTCTGCCGTT ACTGCCCTGT GGGGCAAGG-3'
5-TGCACCTGACTC	CTGTGGAGAA GTCTGCCGTT ACTGCCCTGT GGGGCAAGGT-3'
5-TGCACCTGACTC	

12 met PRIMER

FIG. 50A

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REACTION STOPPED WITH			
ddATP	ddCTP	ddGTP	ddTTP
3581.4 da	3581.4 da 3854.6 da	3581.4 da	3581.4 da
		4488.0 da	4158.9 da
		5120.4 da	4791.2 da
		5448.6 da	
5760.8 da		6089.0 da	
6401.2 da			
6713.4 da		7041.6 da	
	7634.0 da		7344.8 da
		8267.4 da	7938.2 da
	8555.6 da 8844.8 da	9174.0 da	
			9477.2 da 9781.4 da
10094.6 da	10382.8 da		
		11016.2 da	10687.0 da
	11304.4 da 11593.6 da 11652.8 da		
		12516.2 da	12187.0 da
			12819.4 da
		13148.6 da 13476.8 da 13805.0 da 14133.2 da	
	14421.4 da		
14734.6 da		15375.0 da	
15146.8 da		15703.2 da	
			16006.4 da

FIG. 50B

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SEQUENCE OF THE AMPLIFIED 209 bp PCR-PRODUCT OF THE β -GLOBIN GENE

FORWARD PRIMER: β 2
CATTGCTTC TGACACAACT GTGTTCACTA GCAACCTCAA ACAGACACCA
12mer PRIMER
TGGTGCACCT GACTGCTGTG GAGAAGTCTG CCGTTACTGC CCTGTGGGGC
AAGGTGAACG TGGATGAAGT TGGTGGTGAG GCCCTGGGCA GGTGGGTATC
AAGGTTACAA GACAGGTTTA AGGAGACCAA TAGAACTGG GCATGTGGAG
ACAGAGAAG
REVERSE PRIMER β 11

FIG. 51

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5' - gcattcttcttttttactt
3' - cgttagaagagagaaatgaa

1 2 3 4 5 6 7 8 9 10 11 12 13

attt attt attt attt attt attt attt attt attt attt attt attt attt

taaa taaa taaa taaa taaa taaa taaa taaa taaa taaa taaa taaa taaa

g c g c

ttgagacagagctca-3'
aacctgtctcagagt-5'

ALLELE NUMBER OF REPEATS TRUNCATED	THEORETICALLY CALCULATED MOLECULAR MASS	
	ddG	ddG AND ddC
8xAAAT	19440.60	11643.60
9xAAAT	15718.20	21033.60
10xAAAT	16959.00	22274.40
11xAAAT	18199.80	23515.20
12xAAAT	19440.60	24756.00
13xAAAT	20681.40	25996.80
	21922.20	27237.60

FIG. 52

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FIG. 53A

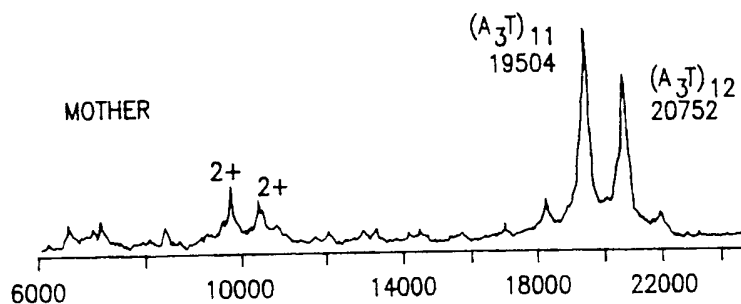


FIG. 53B

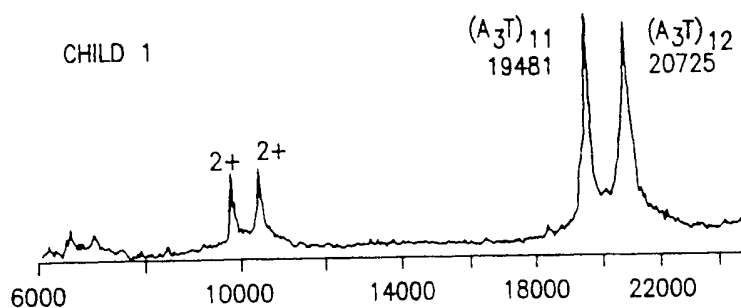


FIG. 53C

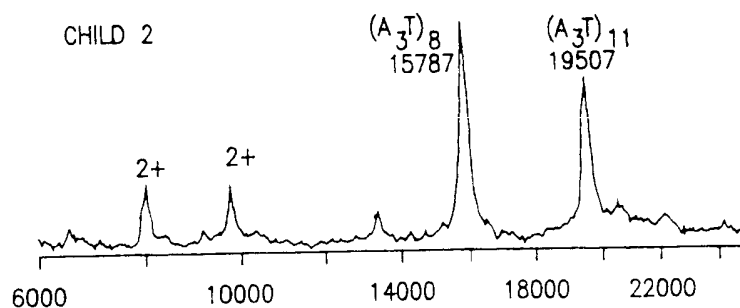


FIG. 53D

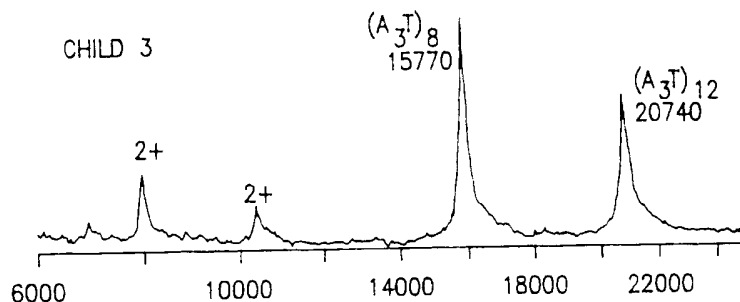
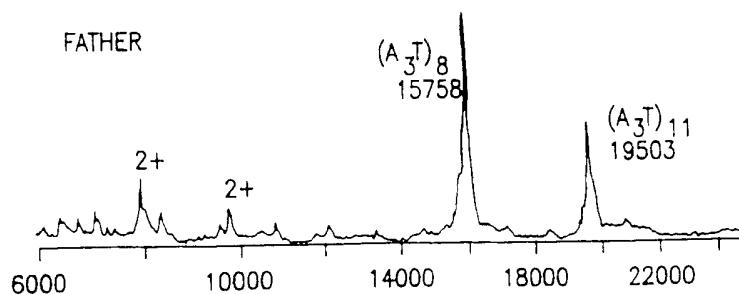


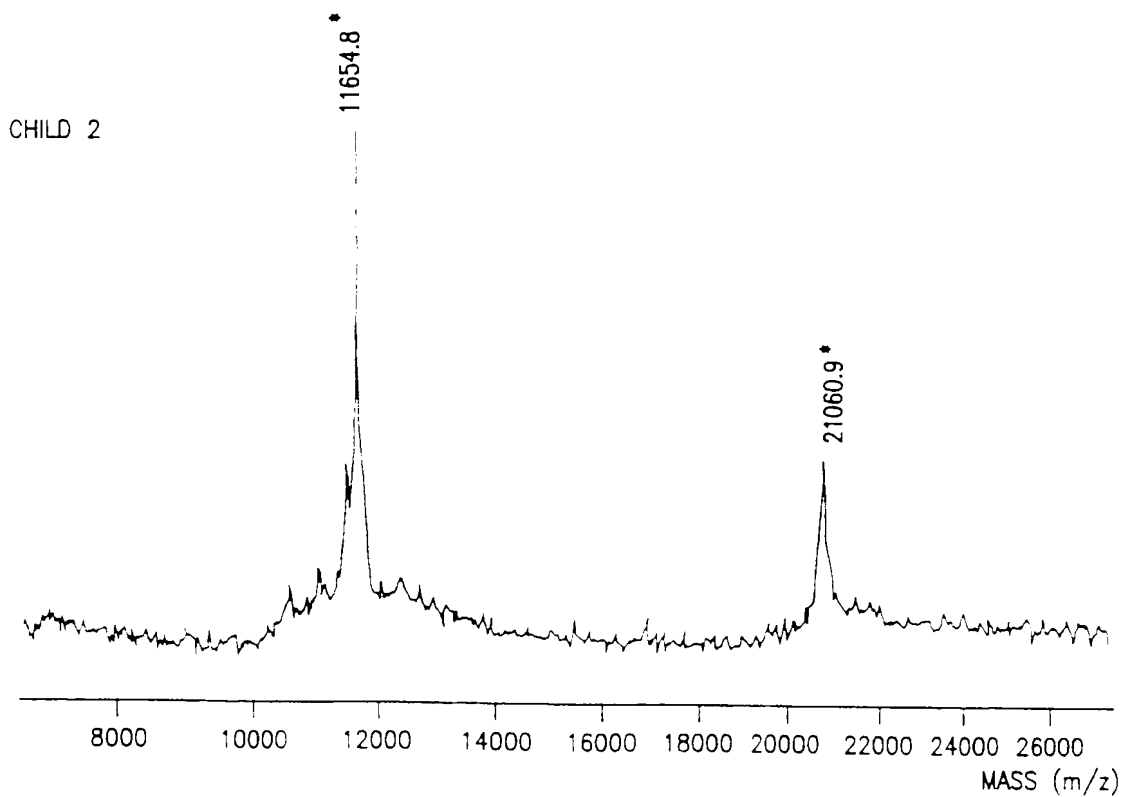
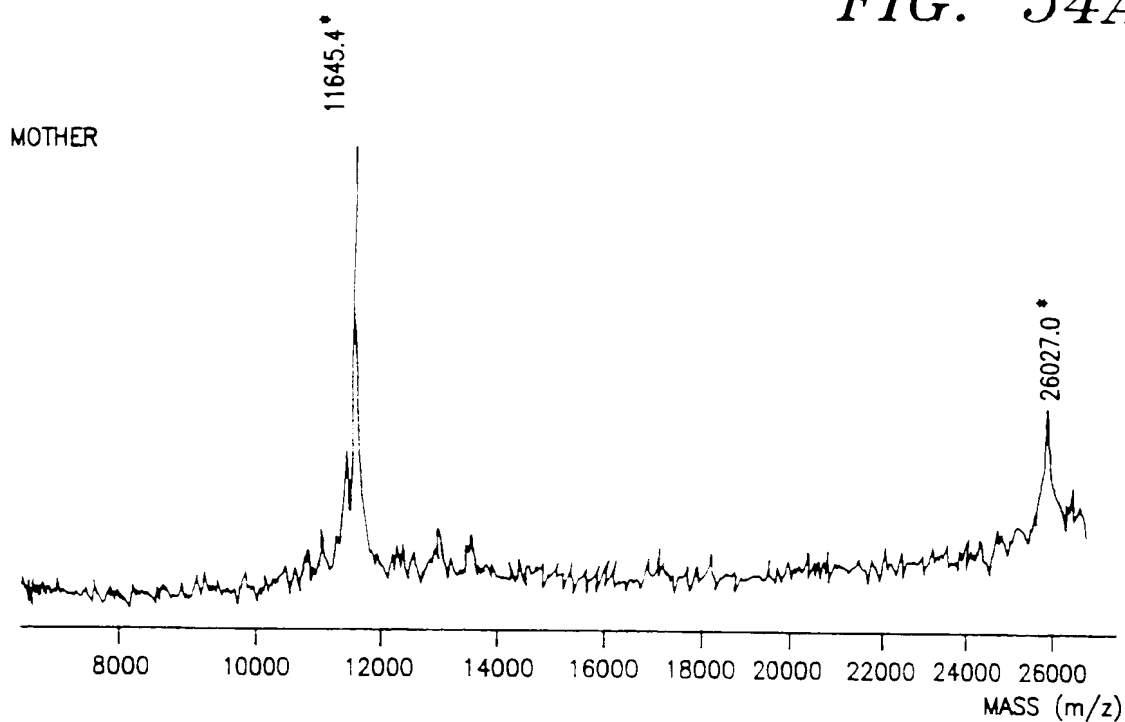
FIG. 53E



SUBSTITUTE SHEET (RULE 26)

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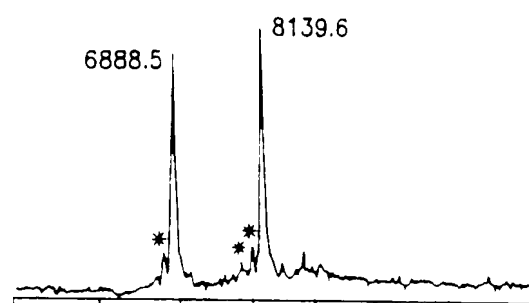
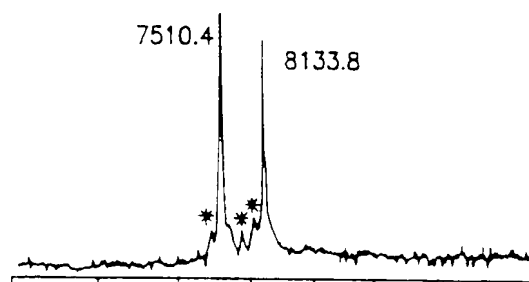
FIG. 54A



SUBSTITUTE SHEET (RULE 26)

5' -GTGTGTGTGTGTGTGTTTTT (TT) (TT) AACAGGGATTGGGGAATTATTGAGA-3'
PRIMER TTGTCCCTAAACCCCTT (4448.0)
T5 ALLELE CAAAAA -- -- TTGTCCCTAAACCCCTT (6890.6)
T7 ALLELE CAAAAA AA -- TTGTCCCTAAACCCCTT (7515.0)
T9 ALLELE CAAAAA AA AA TTGTCCCTAAACCCCTT (8139.4)

FIG. 55

FIG. 56A*FIG. 56B*

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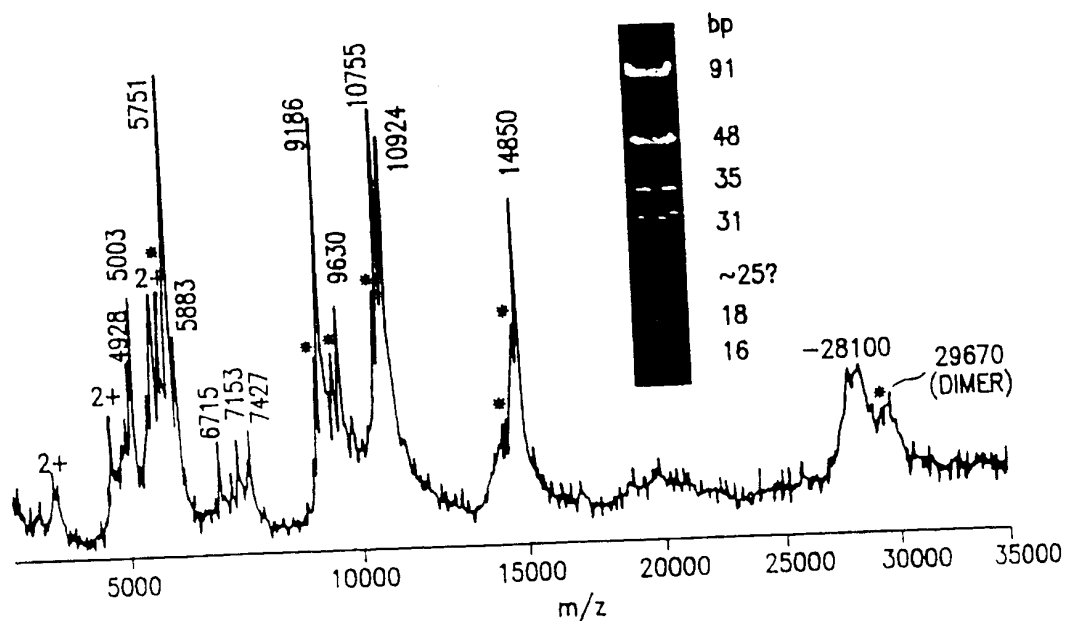


FIG. 57A

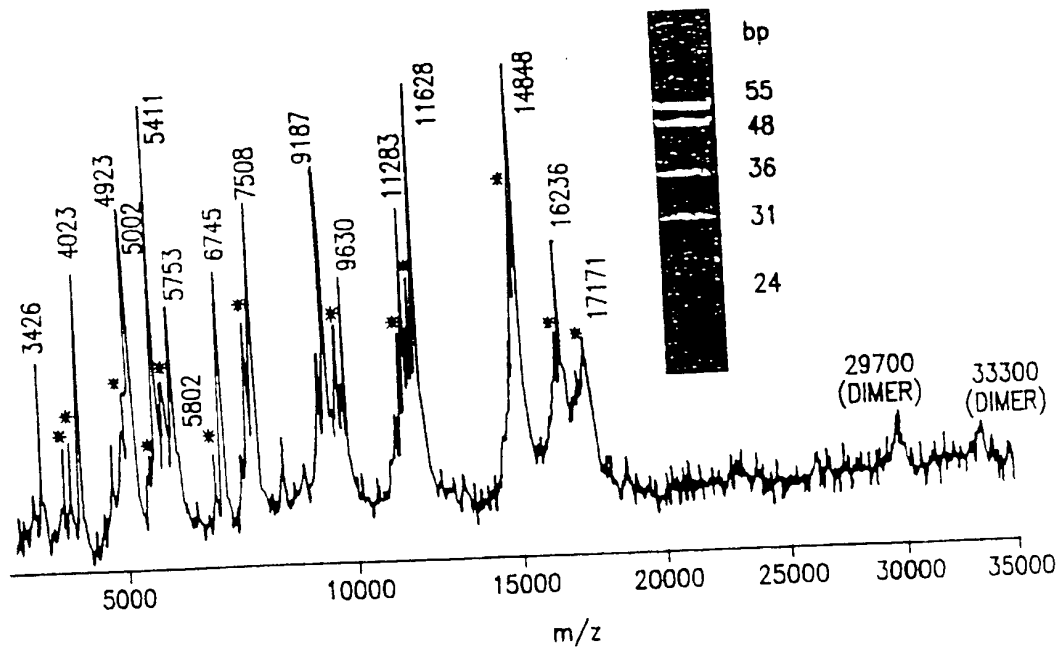


FIG. 57B

SUBSTITUTE SHEET (RULE 26)

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FIG. 58A

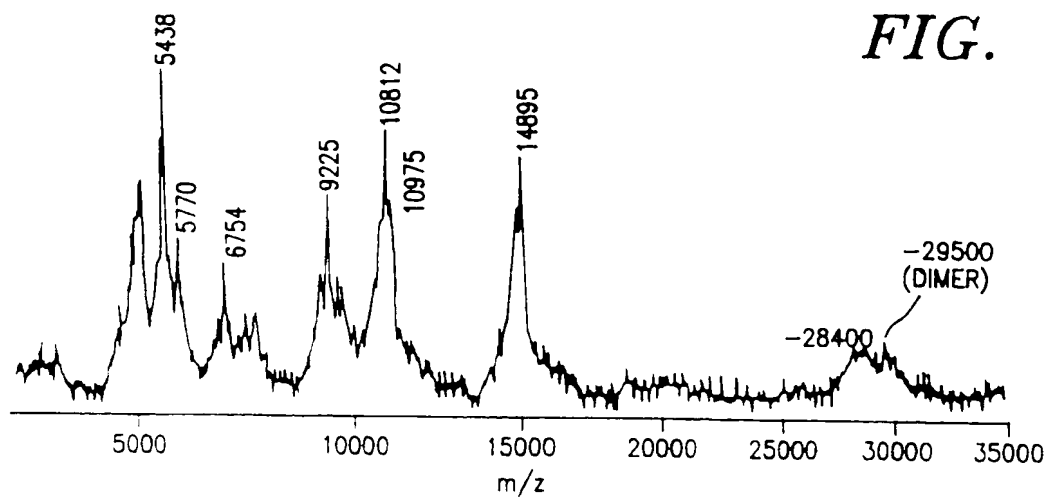


FIG. 58B

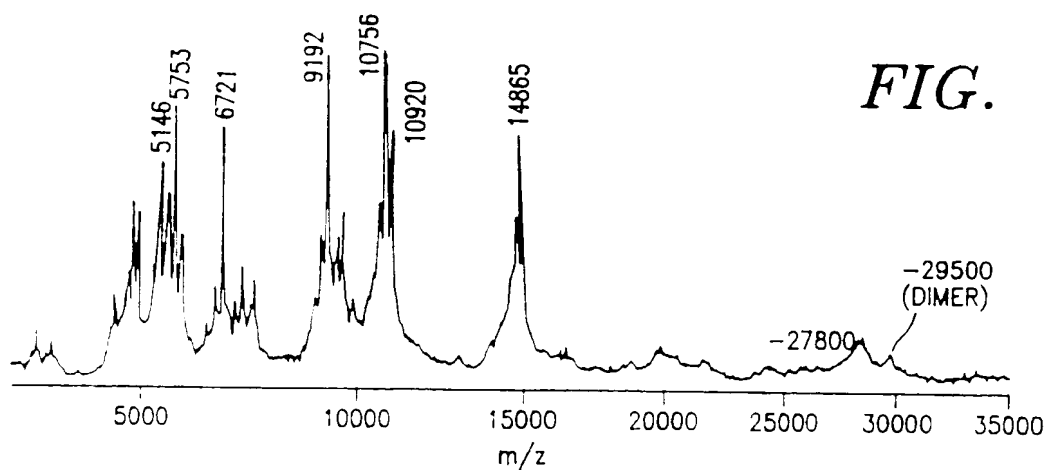
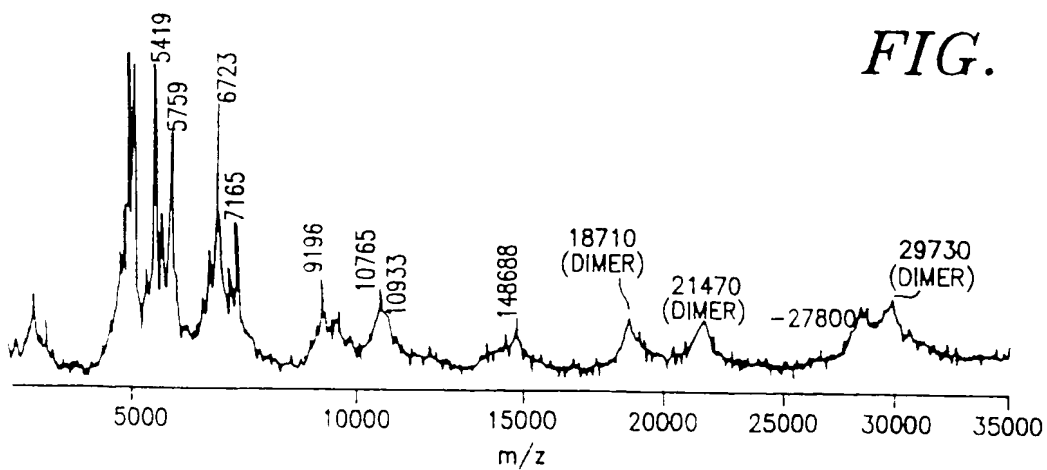


FIG. 58C



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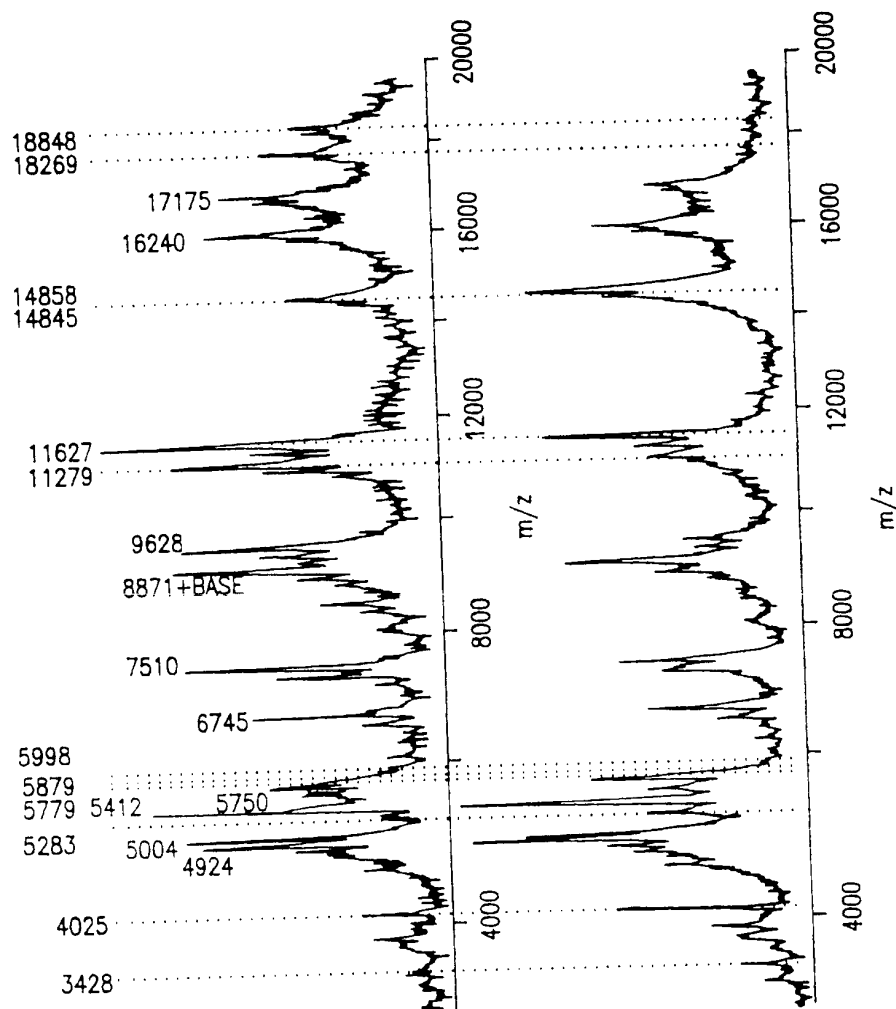


FIG. 59A

FIG. 59B

SUBSTITUTE SHEET (RULE 26)

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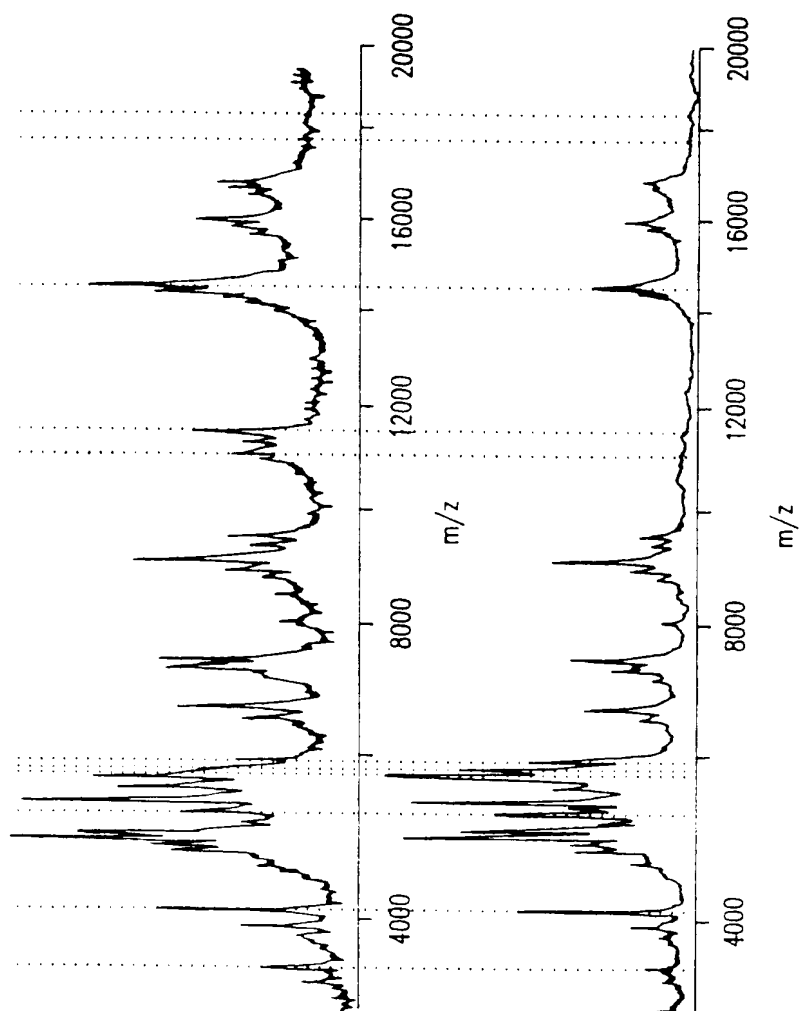


FIG. 59C

FIG. 59D

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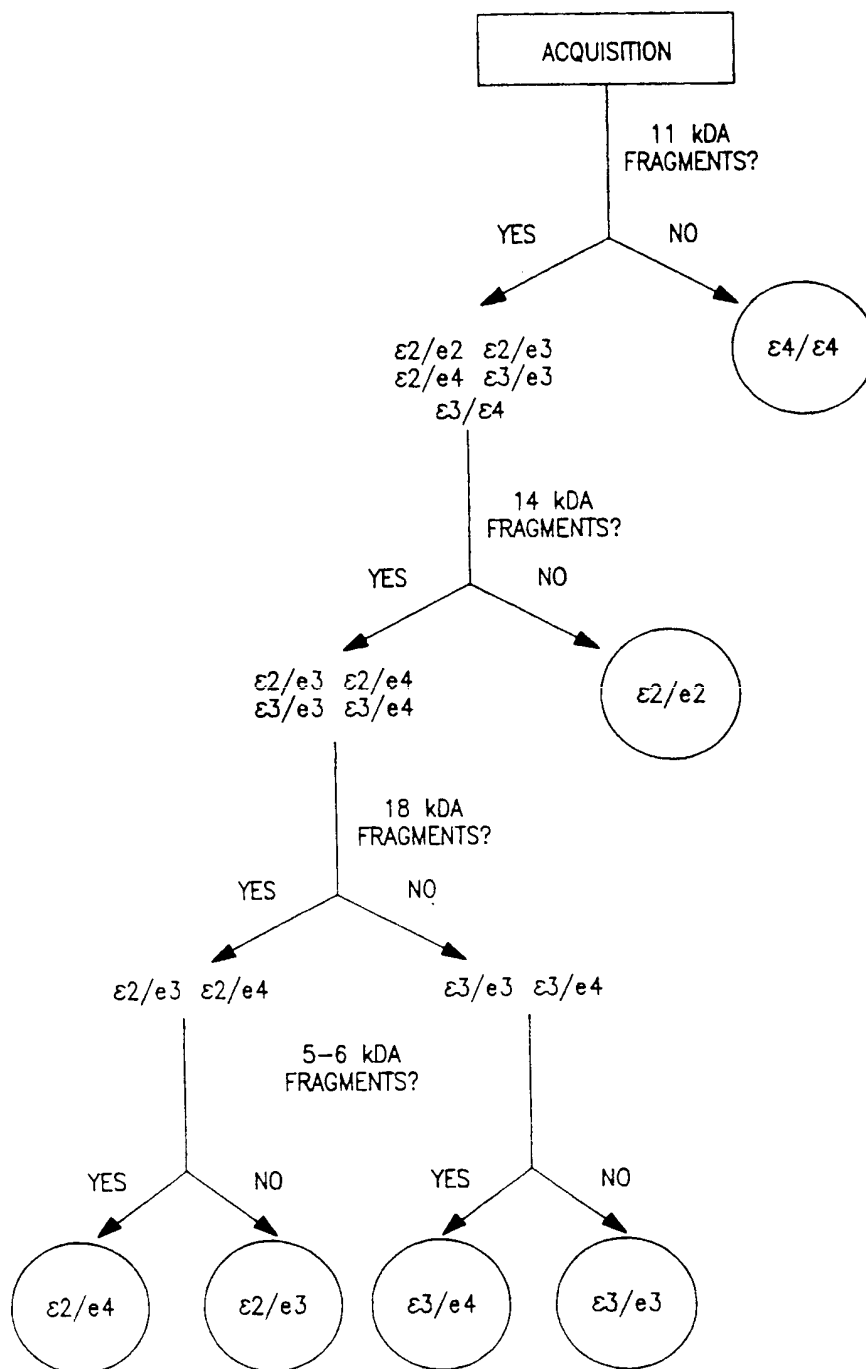


FIG. 60

SUBSTITUTE SHEET (RULE 26)

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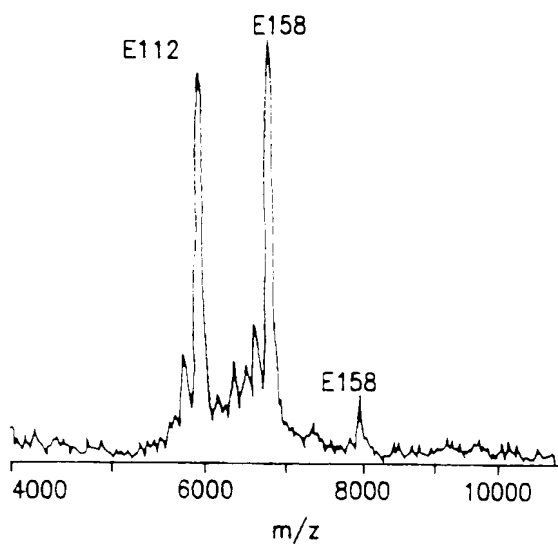
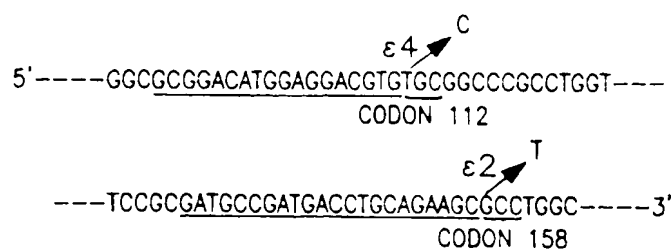


FIG. 61A

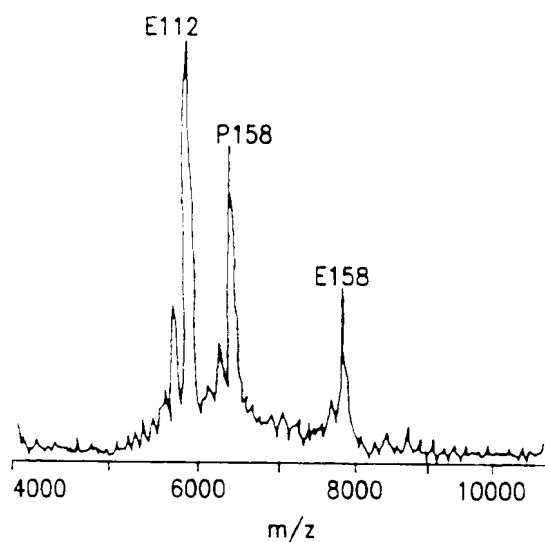
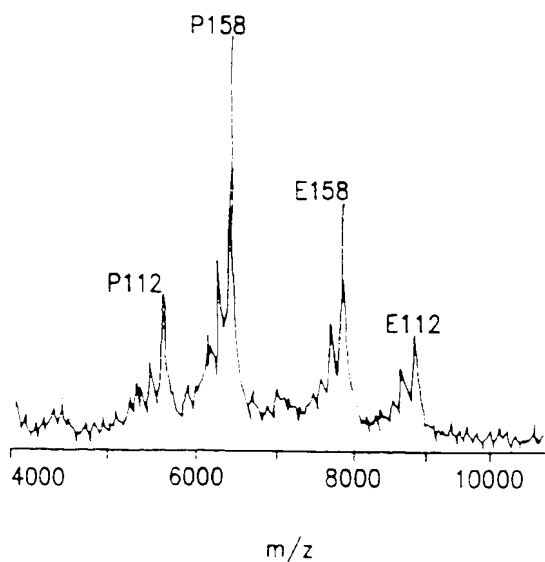
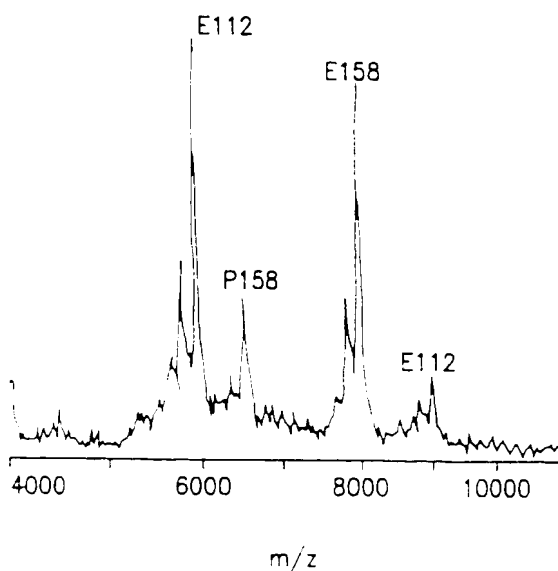


FIG. 61B



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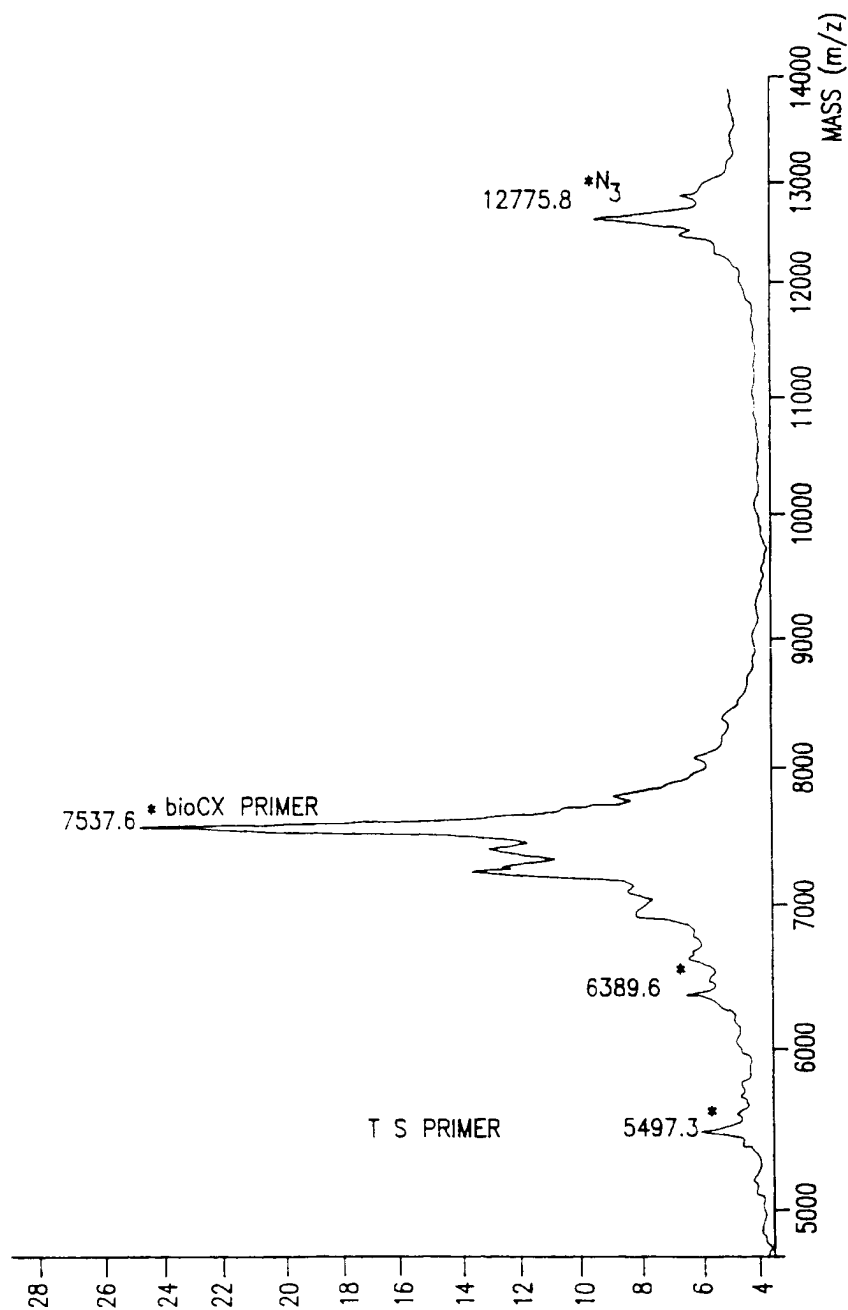


FIG. 62

SUBSTITUTE SHEET (RULE 26)

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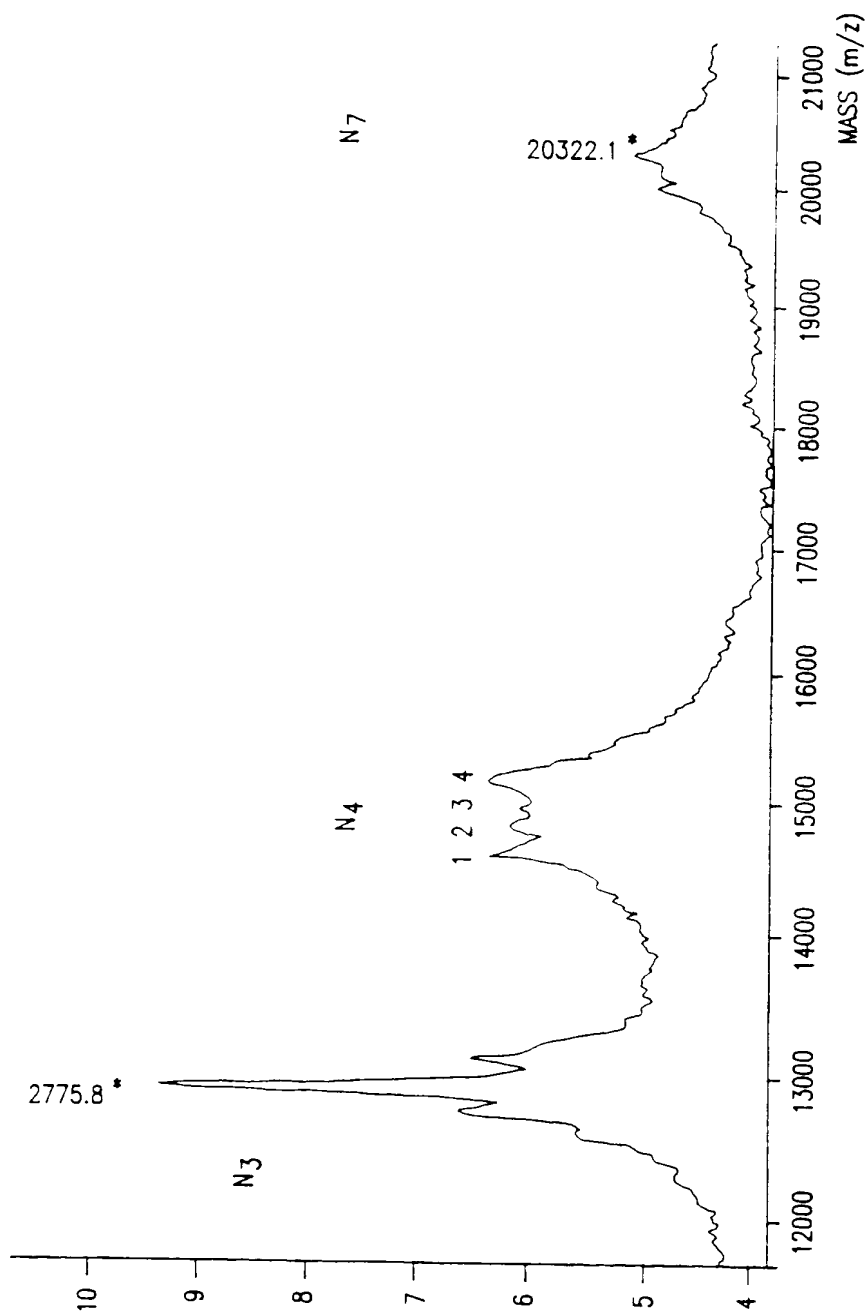


FIG. 63

SUBSTITUTE SHEET (RULE 26)

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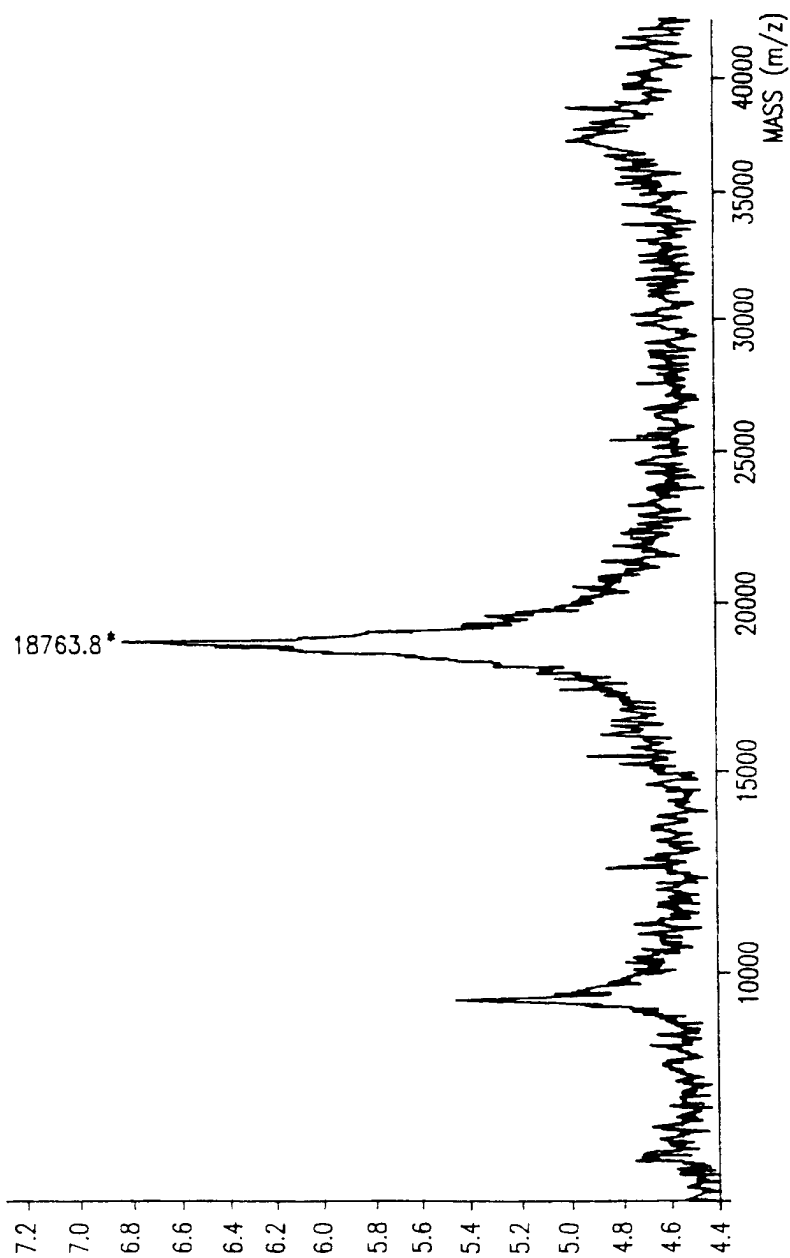


FIG. 64

SUBSTITUTE SHEET (RULE 26)

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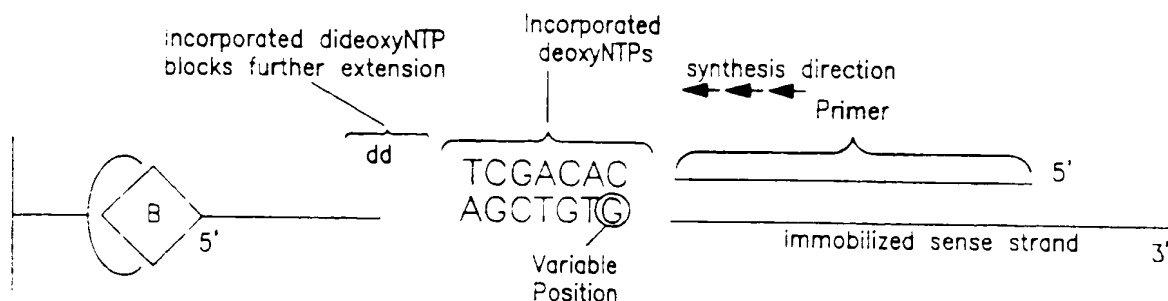


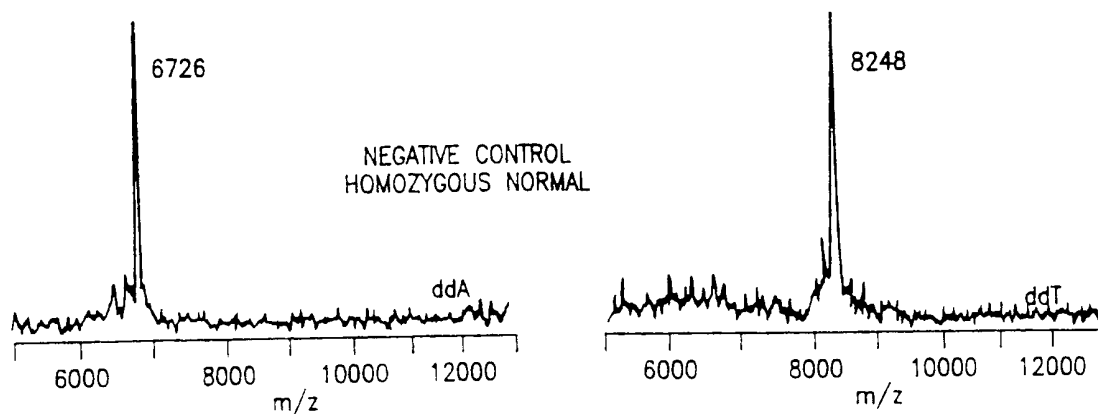
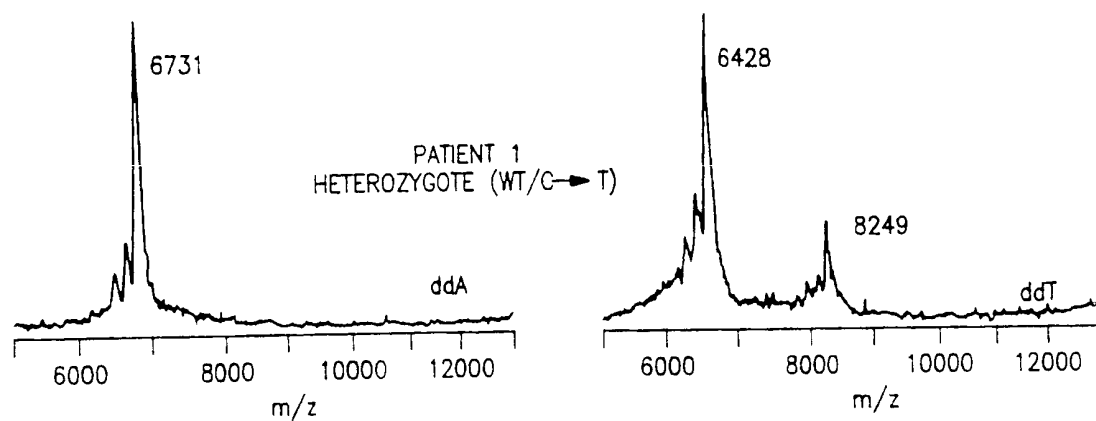
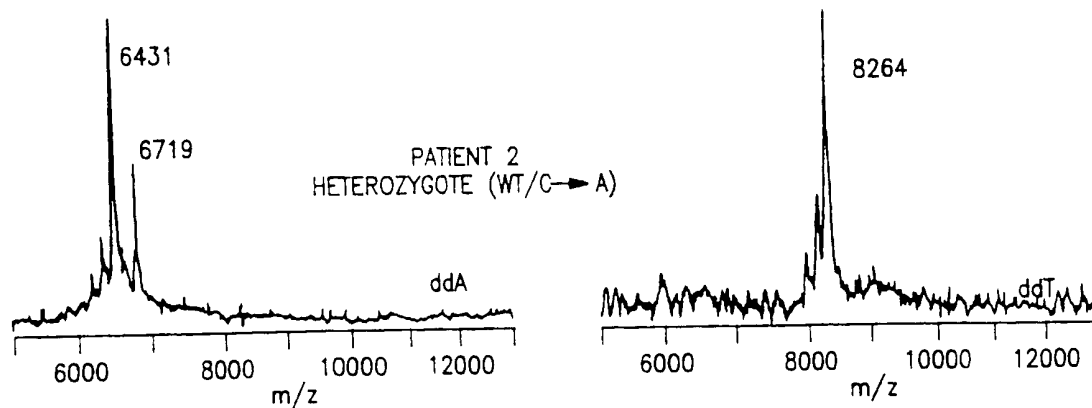
FIG. 65A

ddTTP + dNTP (N=A,C,G)
CGG CTG CGA TCA CCG TGC GG C ACA GCT
 WILDTYPE 8246 Da
CGG CTG CGA TCA CCG TGC GG T
 6423 Da
CGG CTG CGA TCA CCG TGC GG A ACA GCT
 8270 Da

ddATP + dNTP (N=C,T,G)
CGG CTG CGA TCA CCG TGC GG C A
 WILDTYPE 6721 Da
CGG CTG CGA TCA CCG TGC GG T A
 6736 Da
CGG CTG CGA TCA CCG TGC GG A
 6432 Da

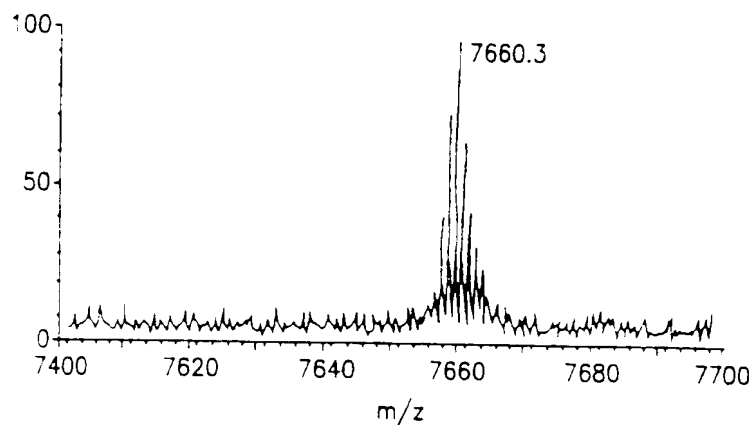
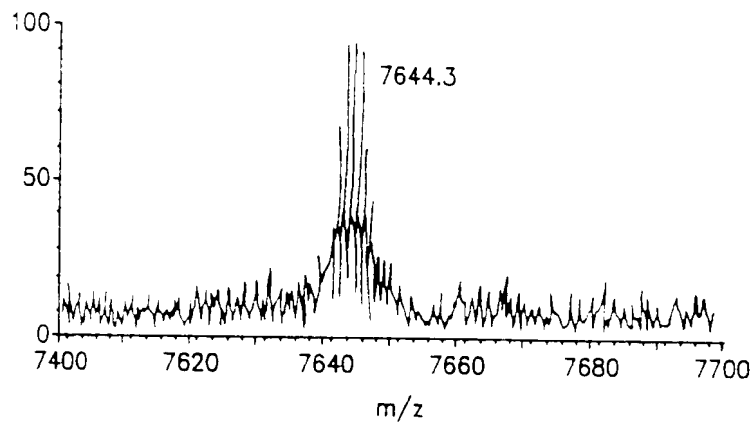
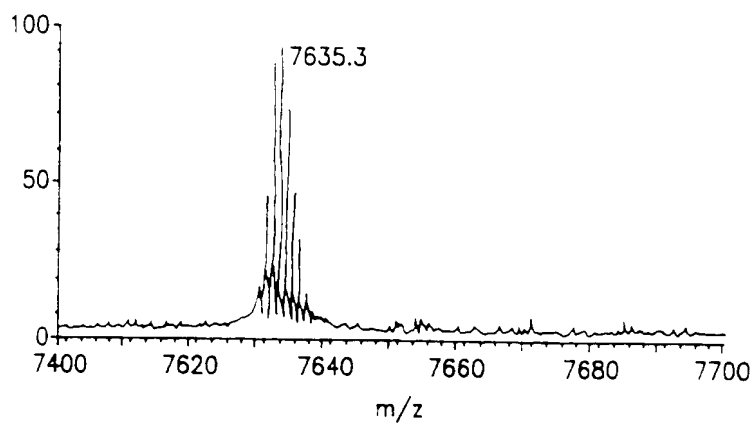
FIG. 65B

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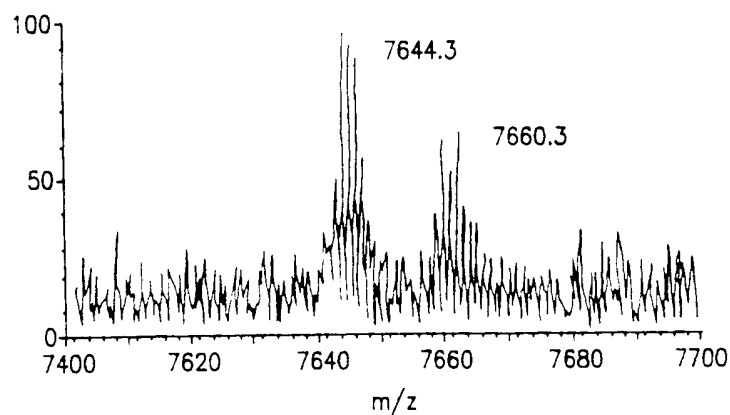
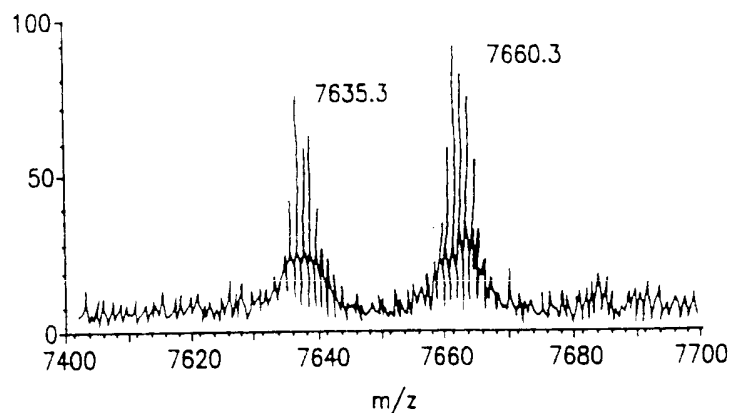
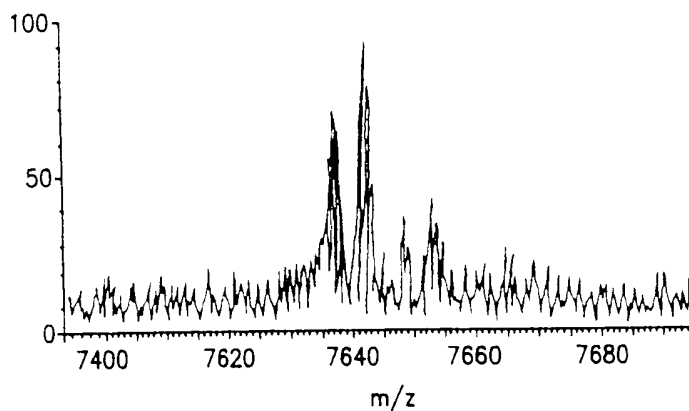
*FIG. 66A**FIG. 66B**FIG. 66C*

SUBSTITUTE SHEET (RULE 26)

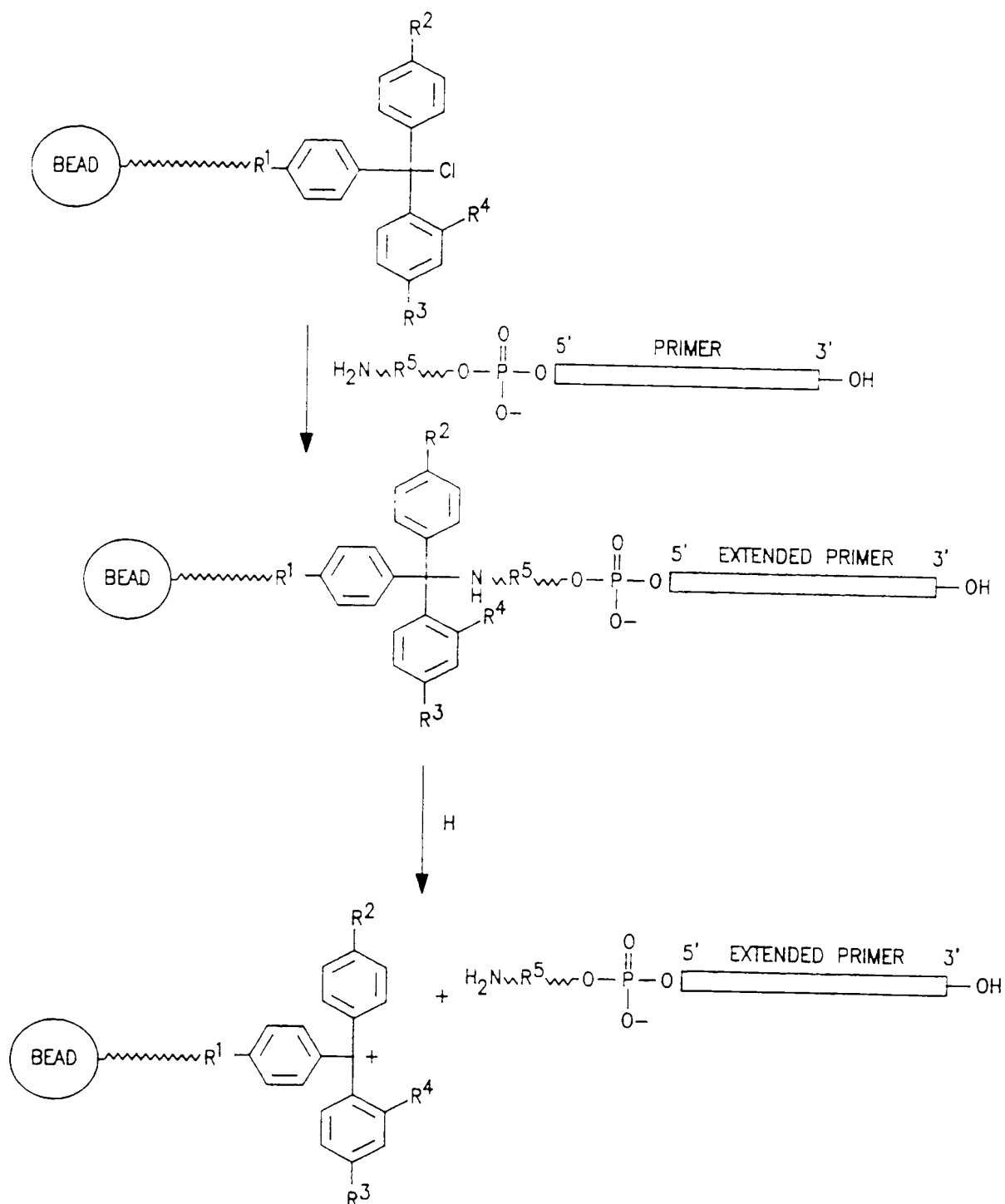
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FIG. 67A*FIG. 67B**FIG. 67C*

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FIG. 67D*FIG. 67E**FIG. 67F*

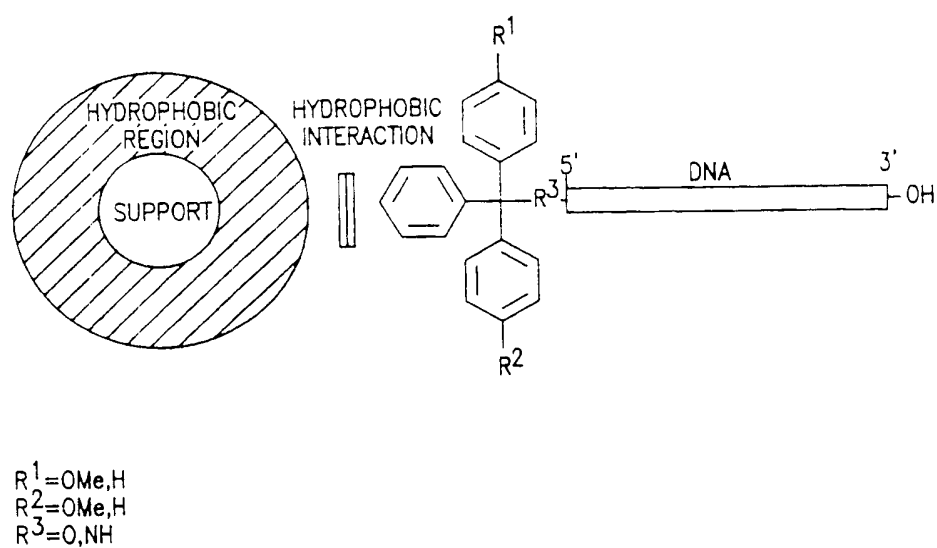
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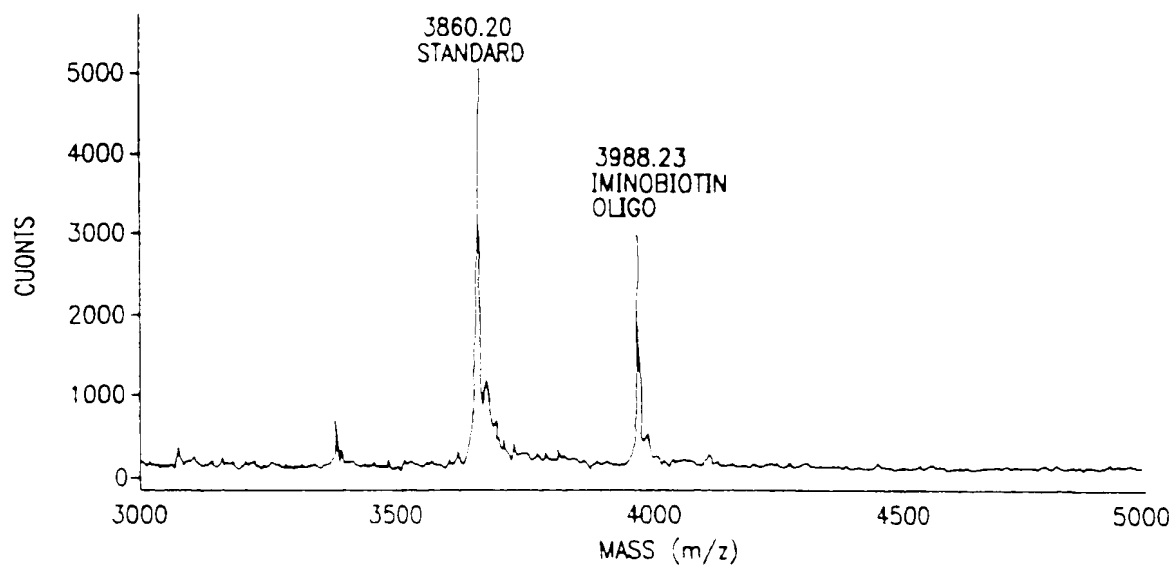
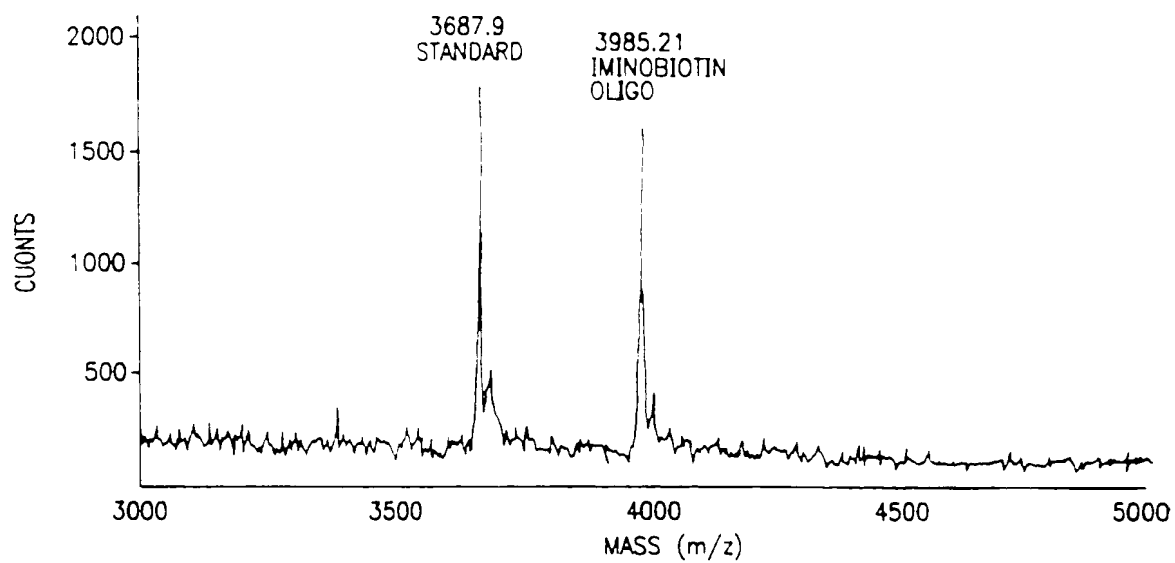
$R^1 = COO-(CH_2)_n$; (PARA OR META)
 $R^2 = MeO; H$
 $R^3 = MeO; H$
 $R^4 = Cl; H$
 $R^5 = (CH_2)_n; (CH_2)_n CONH(CH_2)_n$

FIG. 68

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*FIG. 69*

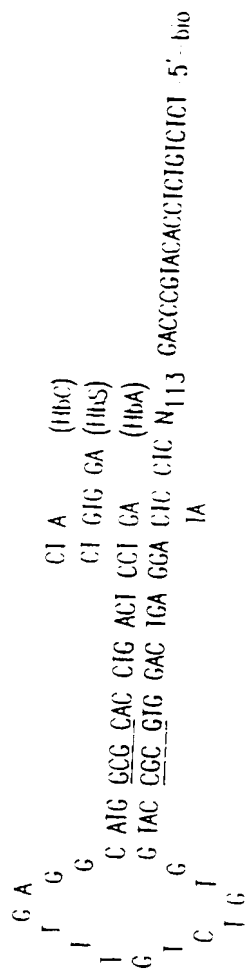
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*FIG. 70**FIG. 71*

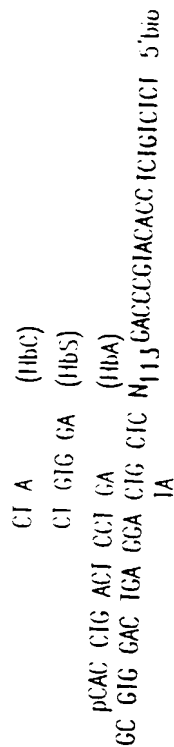
307123

FIG. 72B

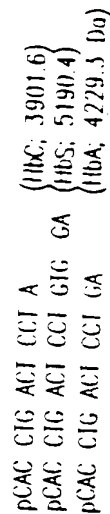
d) PRIMER OLIGO BASE EXTENSION (PROBE) USING ddATP AND dCTP, dGTP, dTTP



e) Cfo I RESTRICTION ENZYME DIGEST



f) MALDI TOF MASS SPEC ANALYSIS



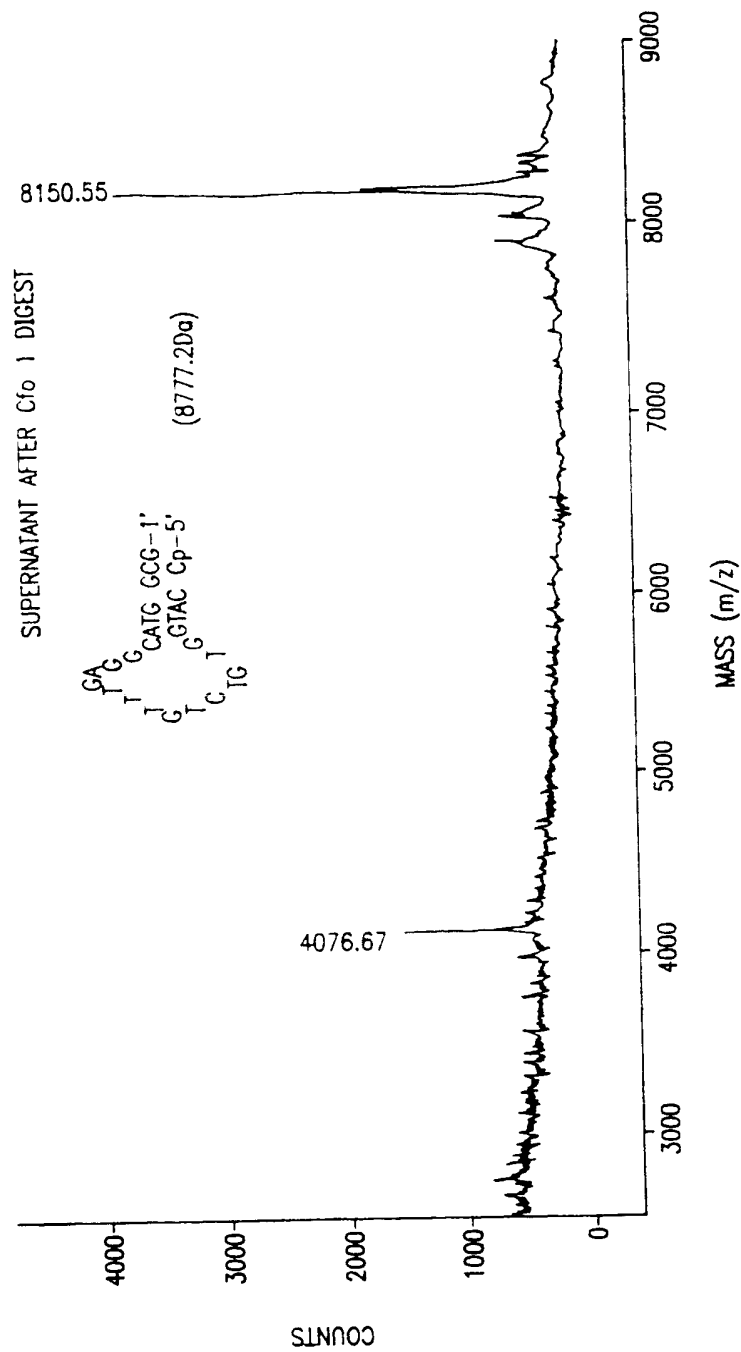


FIG. 73A

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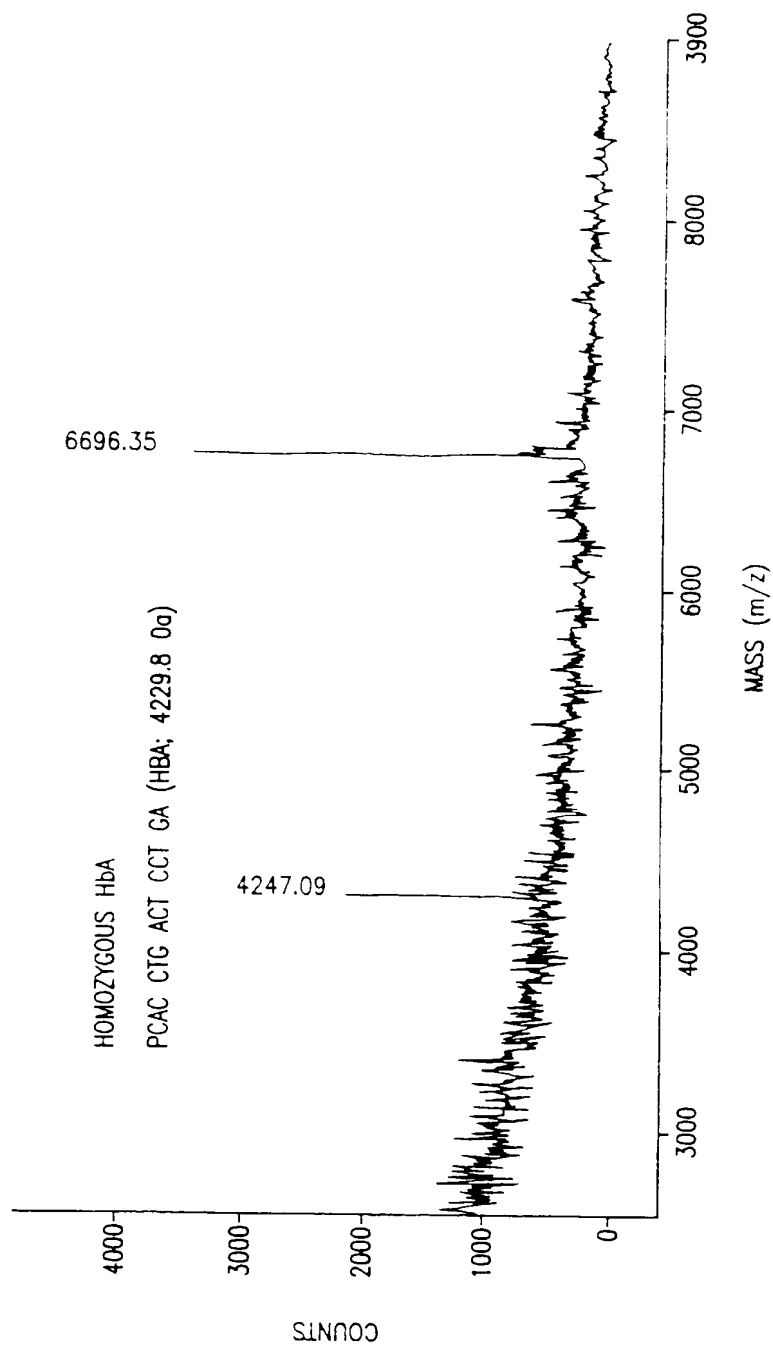


FIG. 73B

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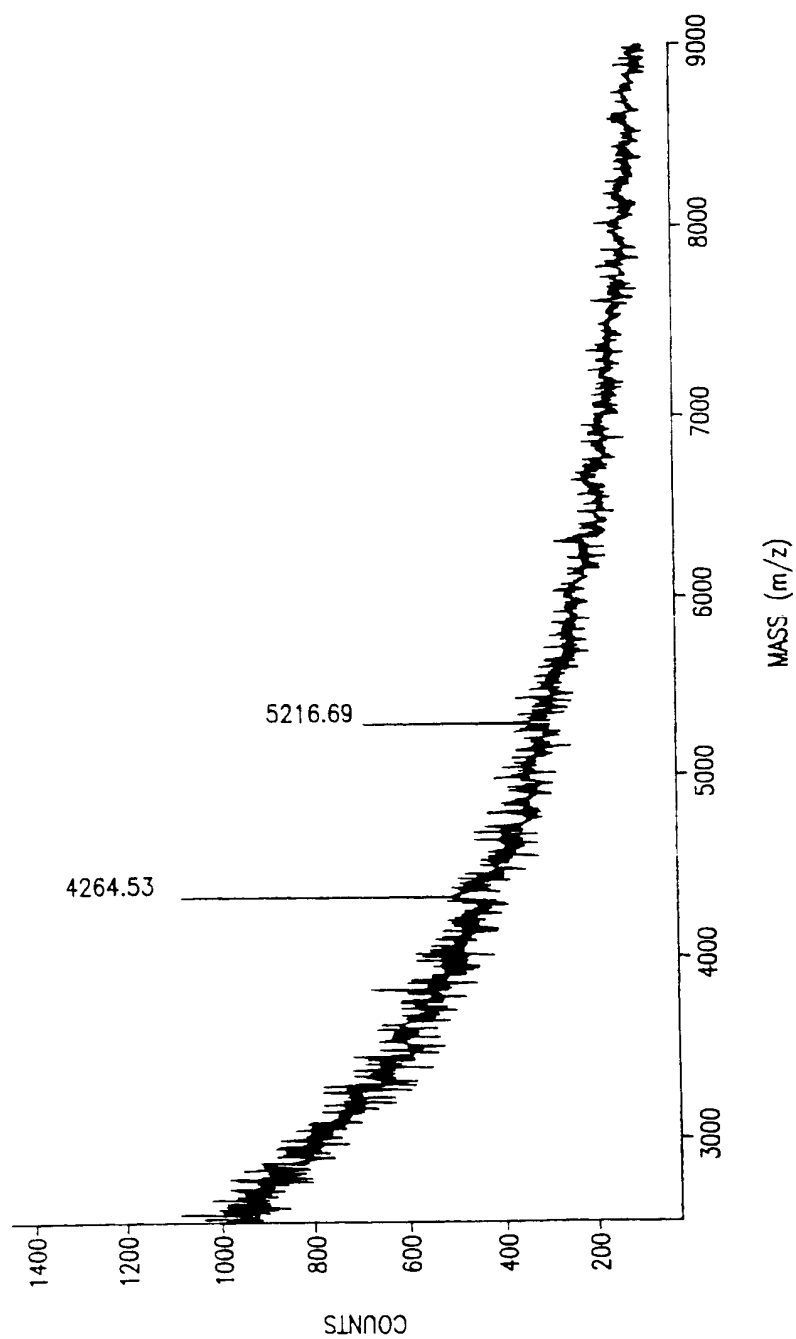
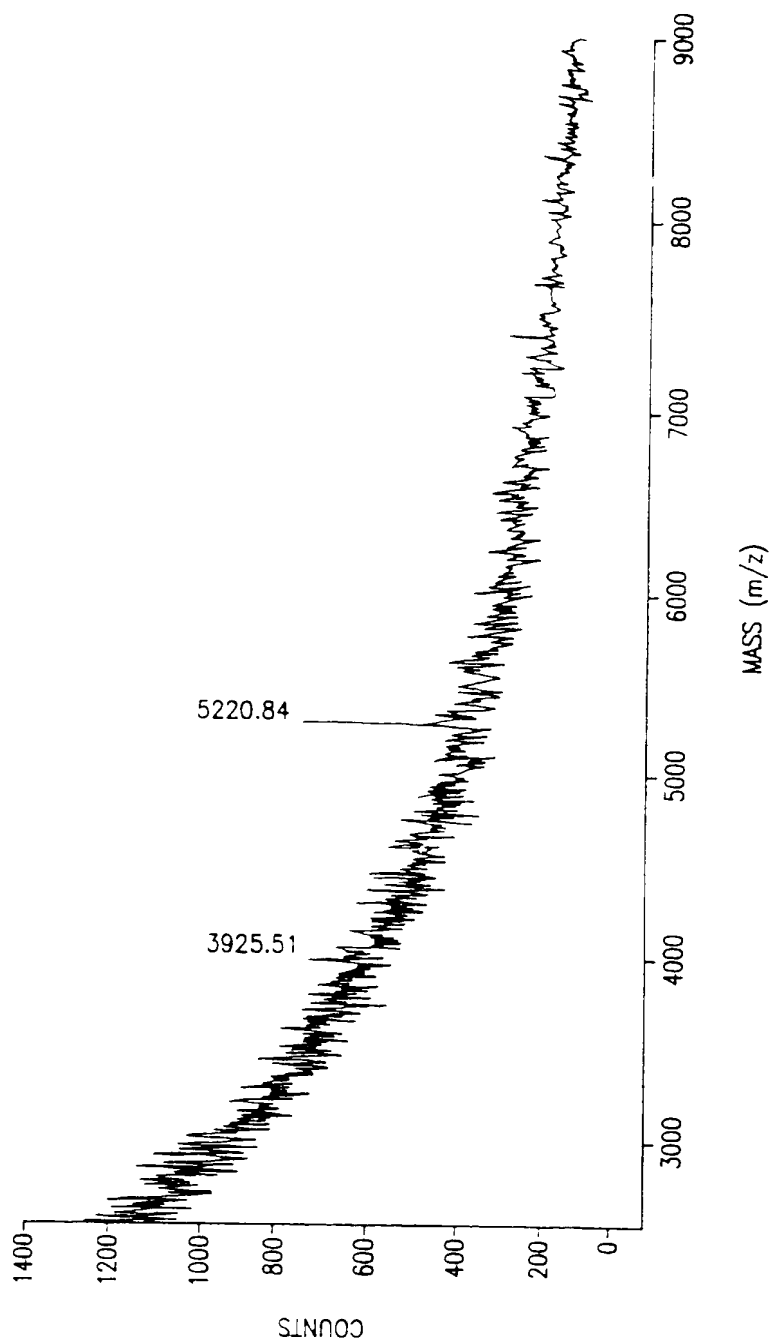


FIG. 73C

SUBSTITUTE SHEET (RULE 26)

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*FIG. 73D*

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5' CAGCTCTCATTTCATACAGTCAGTATCAATTCTGGAAGAATTCAGACATTA
GATAGTCATCTTGGGGCT 3'

FIG. 74

5' ACCTAGCGTTCAGTTCGACTGAGATAATACGACTCATATAGCAGCTCTCATTTCATAC3'
RANDOM SEQUENCE T7 PROMOTER SEQUENCE CKR-5 HOMOLOGUE

FIG. 75

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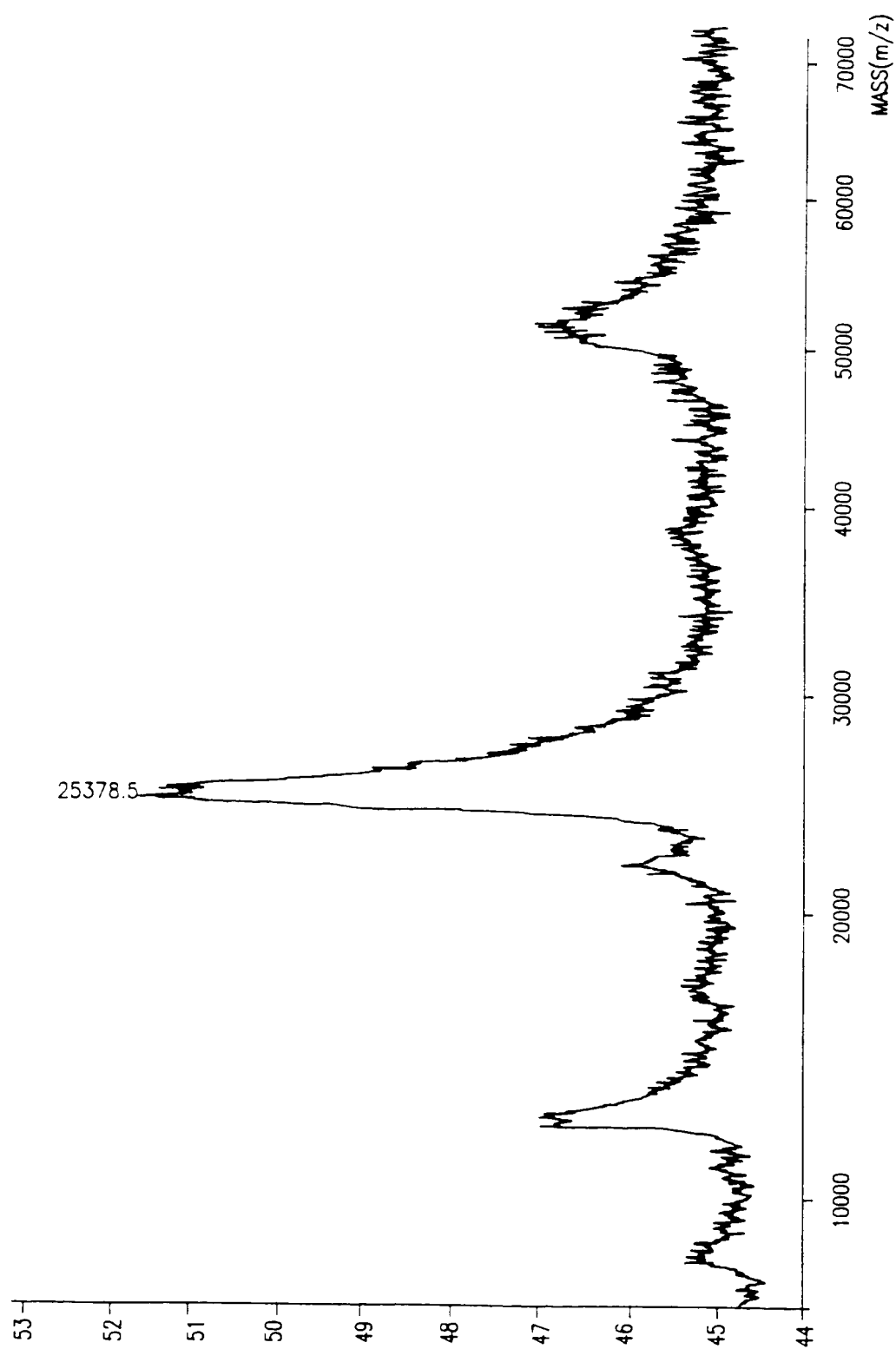


FIG. 76

SUBSTITUTE SHEET (RULE 26)

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FIG. 77A

RNase T₁
GpN →

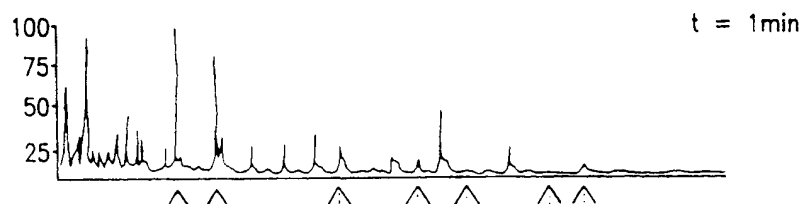


FIG. 77B

ALKALINE
HYDROLYSIS

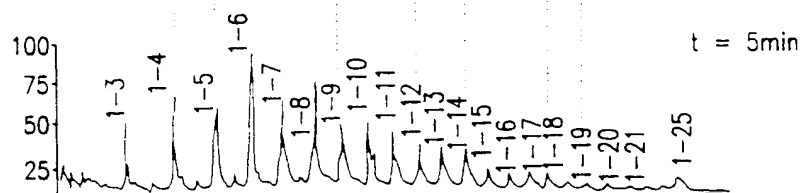


FIG. 77C

U₂
ApN →

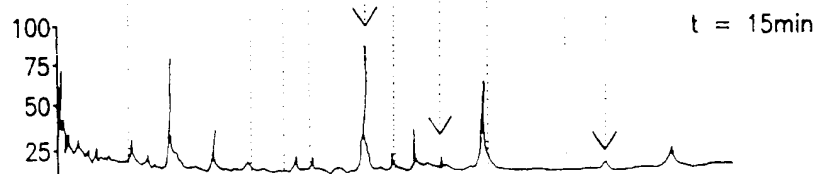


FIG. 77D

PhyM
ApN →
UpN →

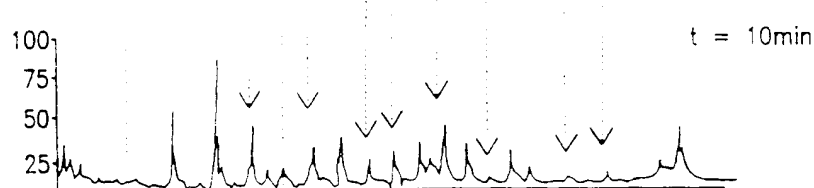
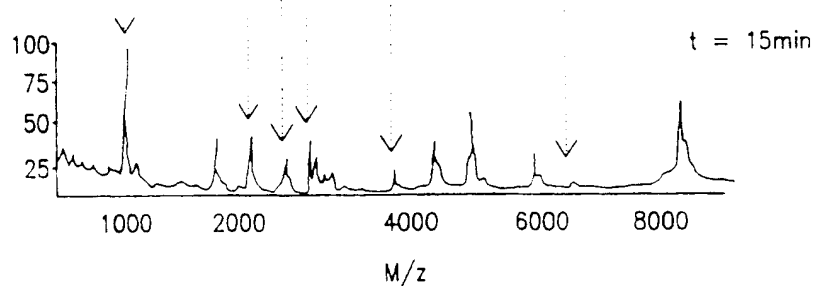


FIG. 77E

A
UpN →
GpN →



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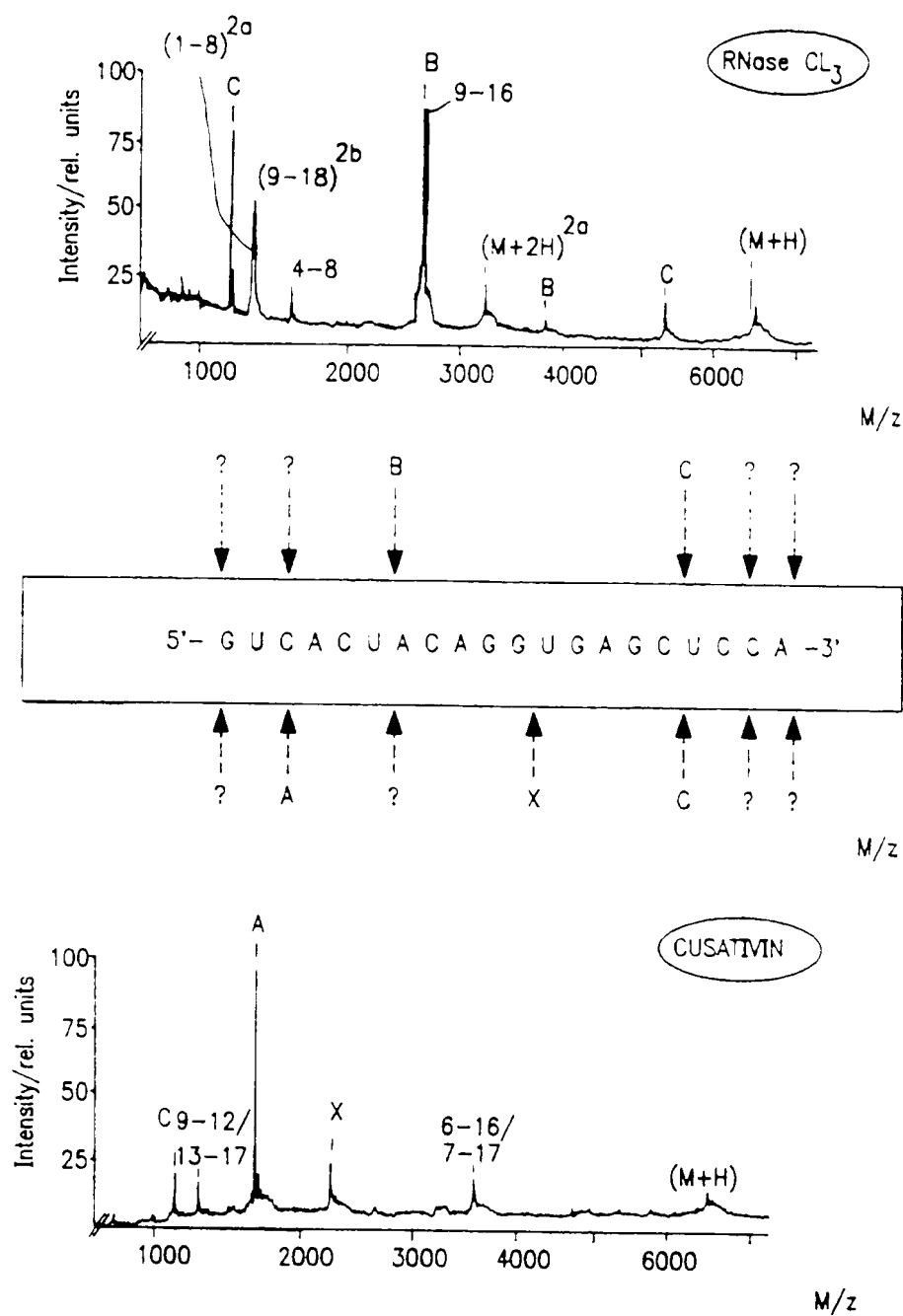


FIG. 78

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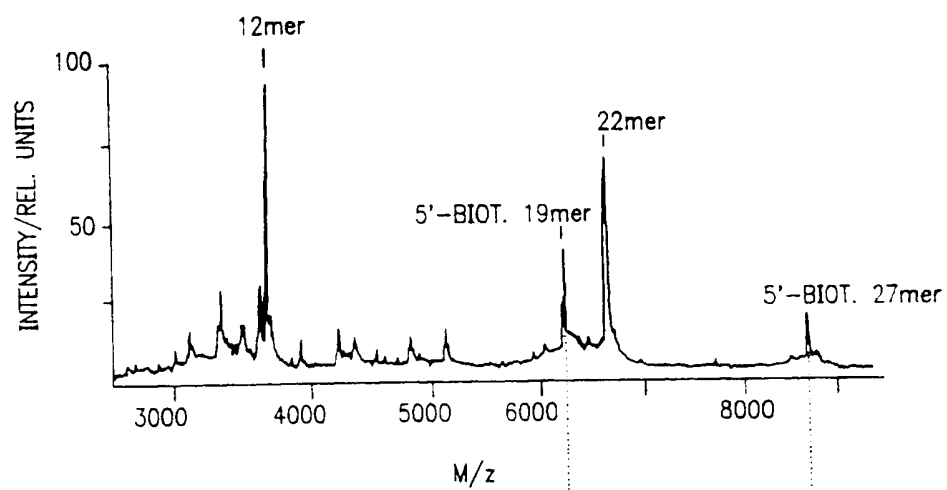


FIG. 79A

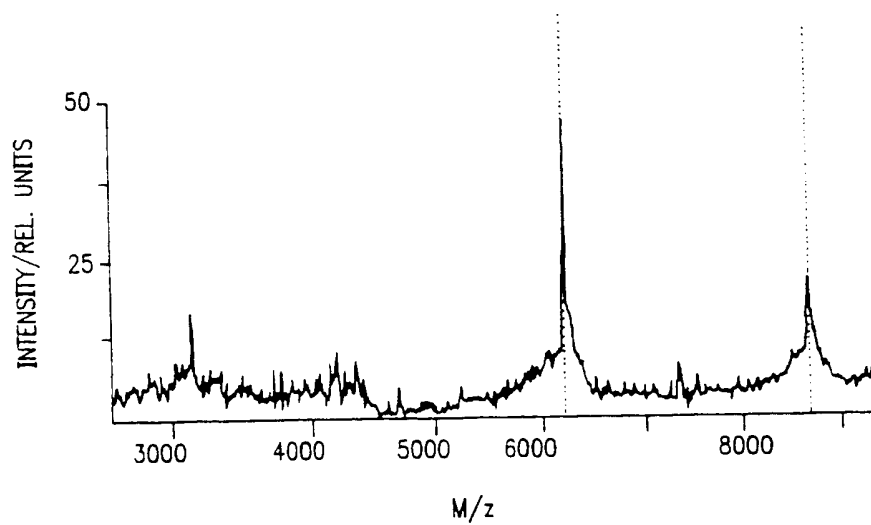
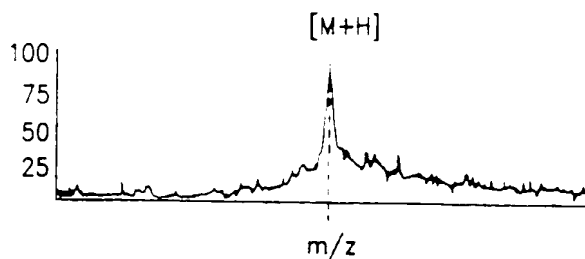
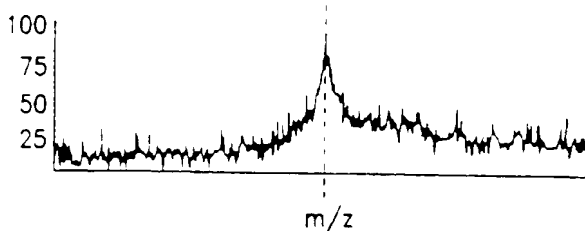
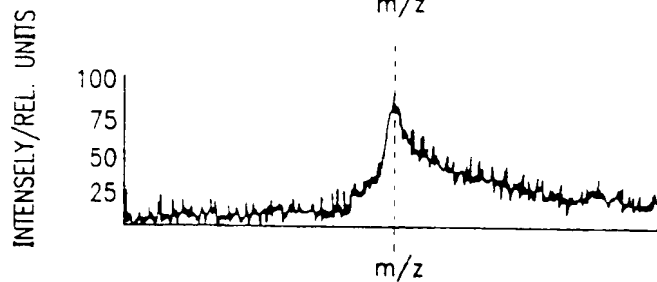
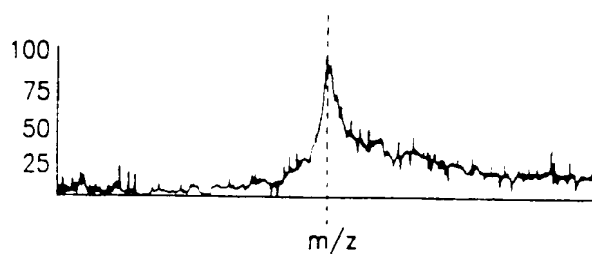
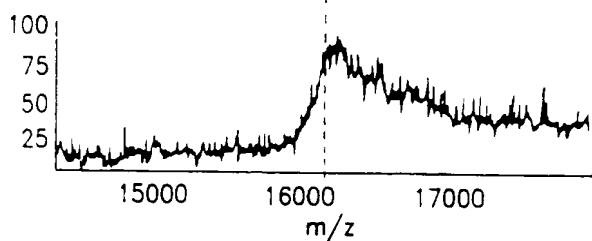


FIG. 79B

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FIG. 80A*FIG. 80B**FIG. 80C**FIG. 80D**FIG. 80E*

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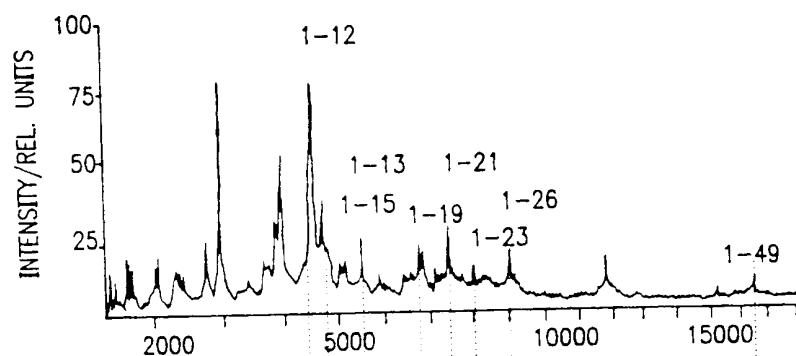
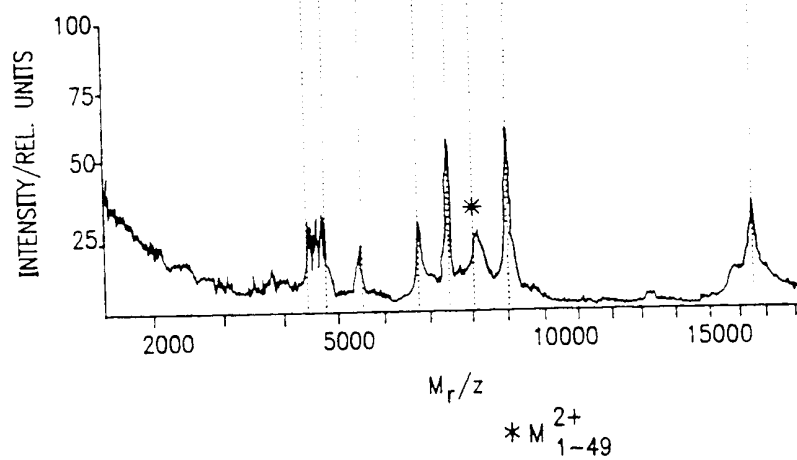
*FIG. 81A**FIG. 81B*

FIG. 82A

β -2
 CATTGCTTC TCACACAAC TGTGTCAC TAA GGAACCTCA
 GTCGTCCTC
 β -TAG1
 GTCGTCCC ATG GTG CAC CTG ACT C
 1 2 3 4 5 6 7 8 (CODON)
 ACACACACC ATG GTG CAC CTG ACT CCT GAG CAG AAG ICT GCC GTT
 -CT
 THALASSEMIA (COD5 Δ CT)
 A HbC ---
 T HbS

β -TAG2
 CGCTGTGGT GAG GCC CTG GGC A
 27 28 29 30 (CODON)
 ACT GCC CTG TGG GGC AAG GTG AAC GTG GAT GAA GTT GGT GGT GAG GCC CTG GGC AG GTGGTAICA AGGTACAAG
 A
 THALASSEMIA (IVS -1 nt1 G>A)
 C THALASSEMIA (IVS -1 nt5 G>C)
 CTHALASSEMIA (IVS -1 nt6 T>C)

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ACAGGTTTAA GGAGACCAAT AGAACTGGG CATGTGGAGA CAGAGAAG
 β -11

FIG. 82B

(1) SINGLE STRANDED
 (STV) BIO3' - ACCTCAGTCCATCGTCAGCAGCAG - 5'
 UNIVERSAL SS SEQUENCE | COMPLEMENTARY
 E.G. β -TAG1

(2) PARTLY DOUBLE STRANDED
 5'-TGGAGTCAGGTAGCAGTC-3'
 (STV) BIO 3'-ACCTCAGTCCATCGTCAGCAGCAG - 5'
 UNIVERSAL DS SEQUENCE | COMPLEMENTARY
 E.G. β -TAG2

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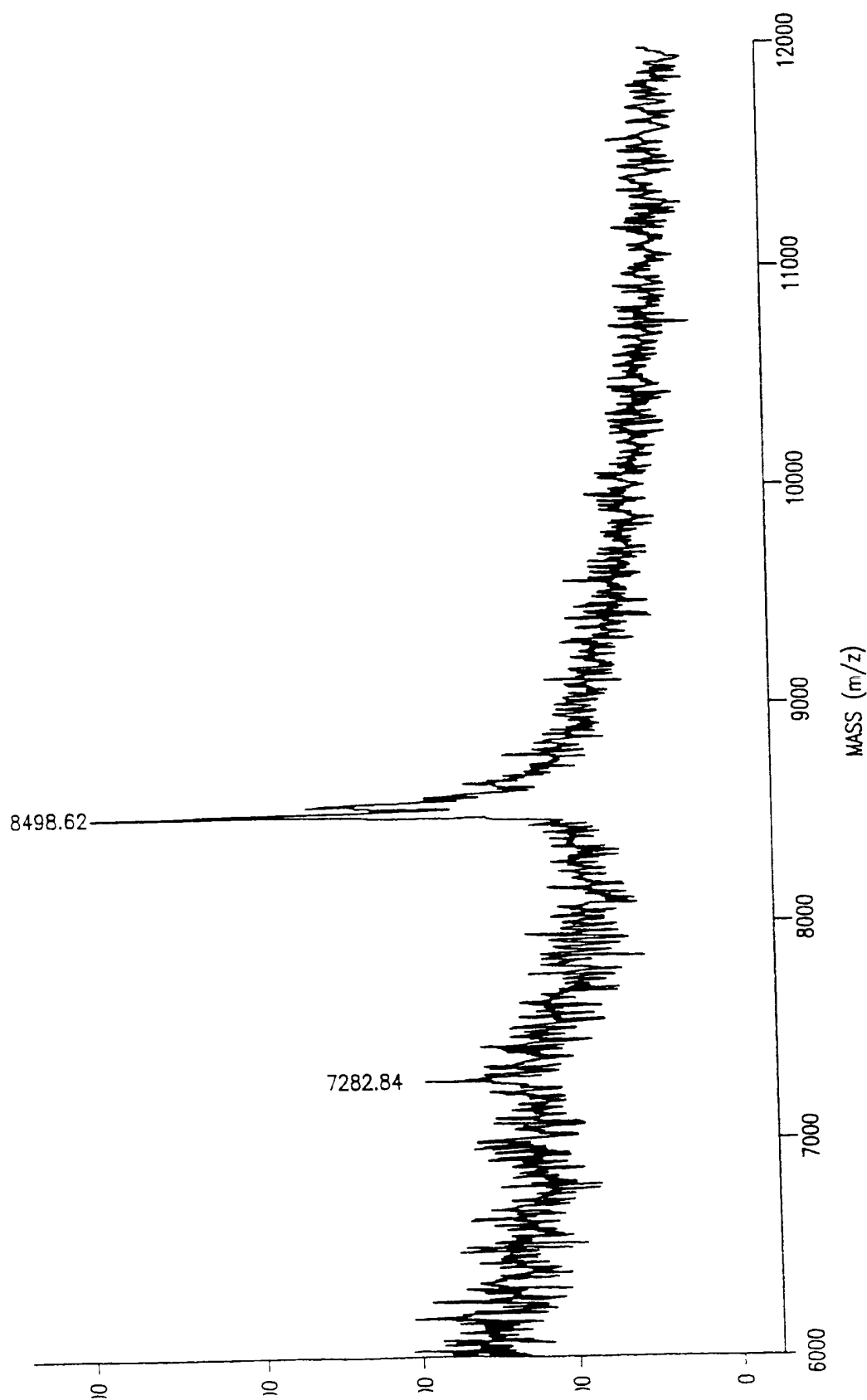


FIG. 83

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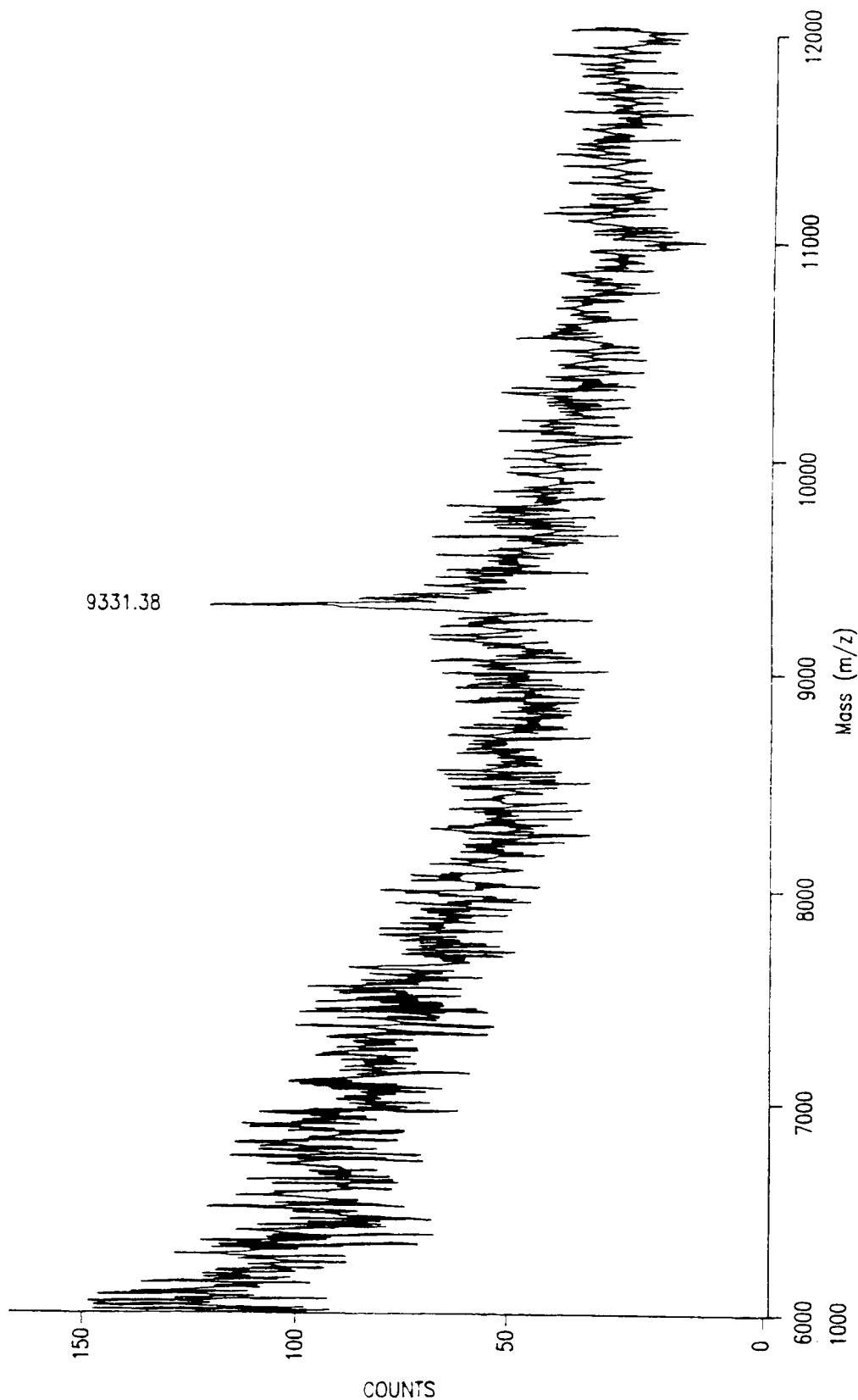


FIG. 84

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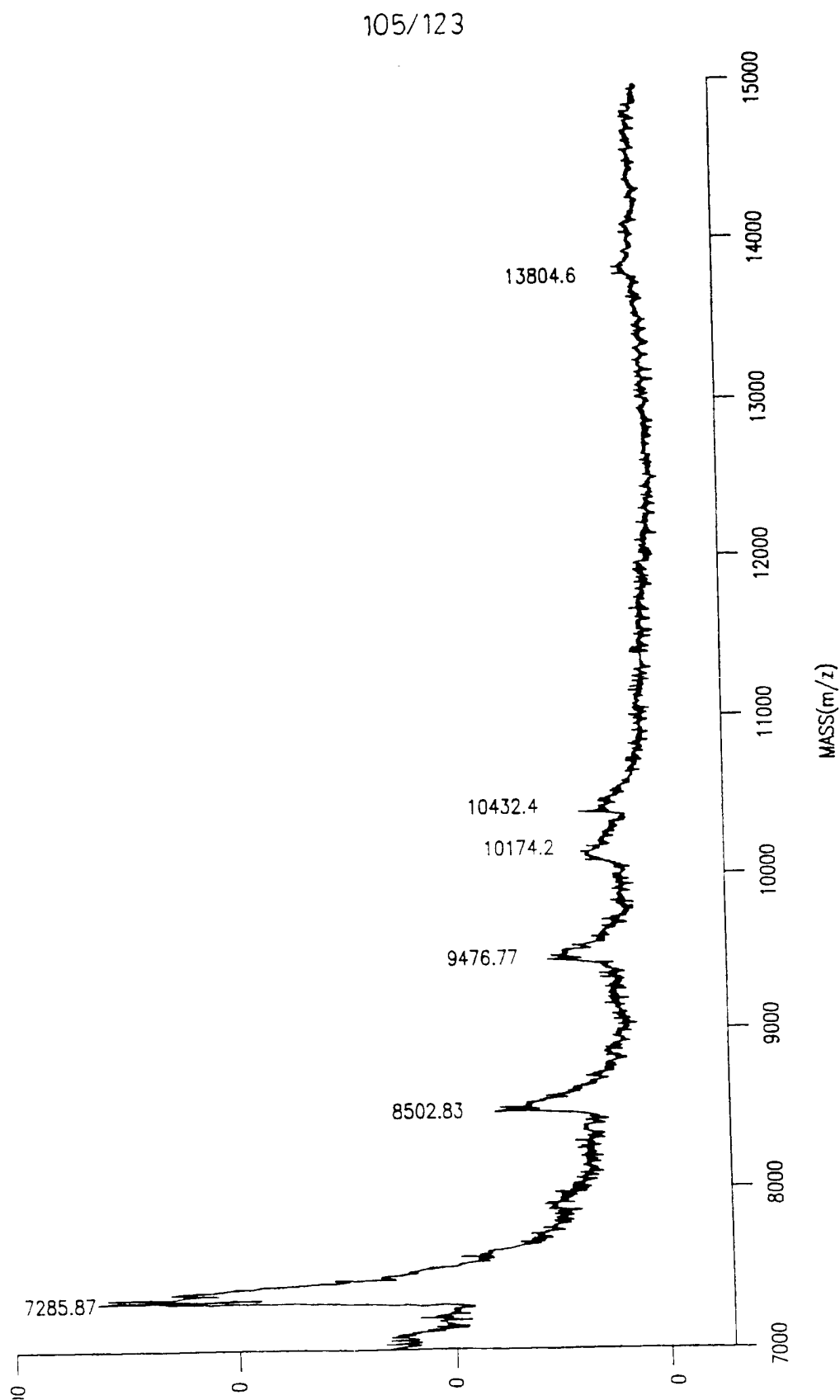


FIG. 85

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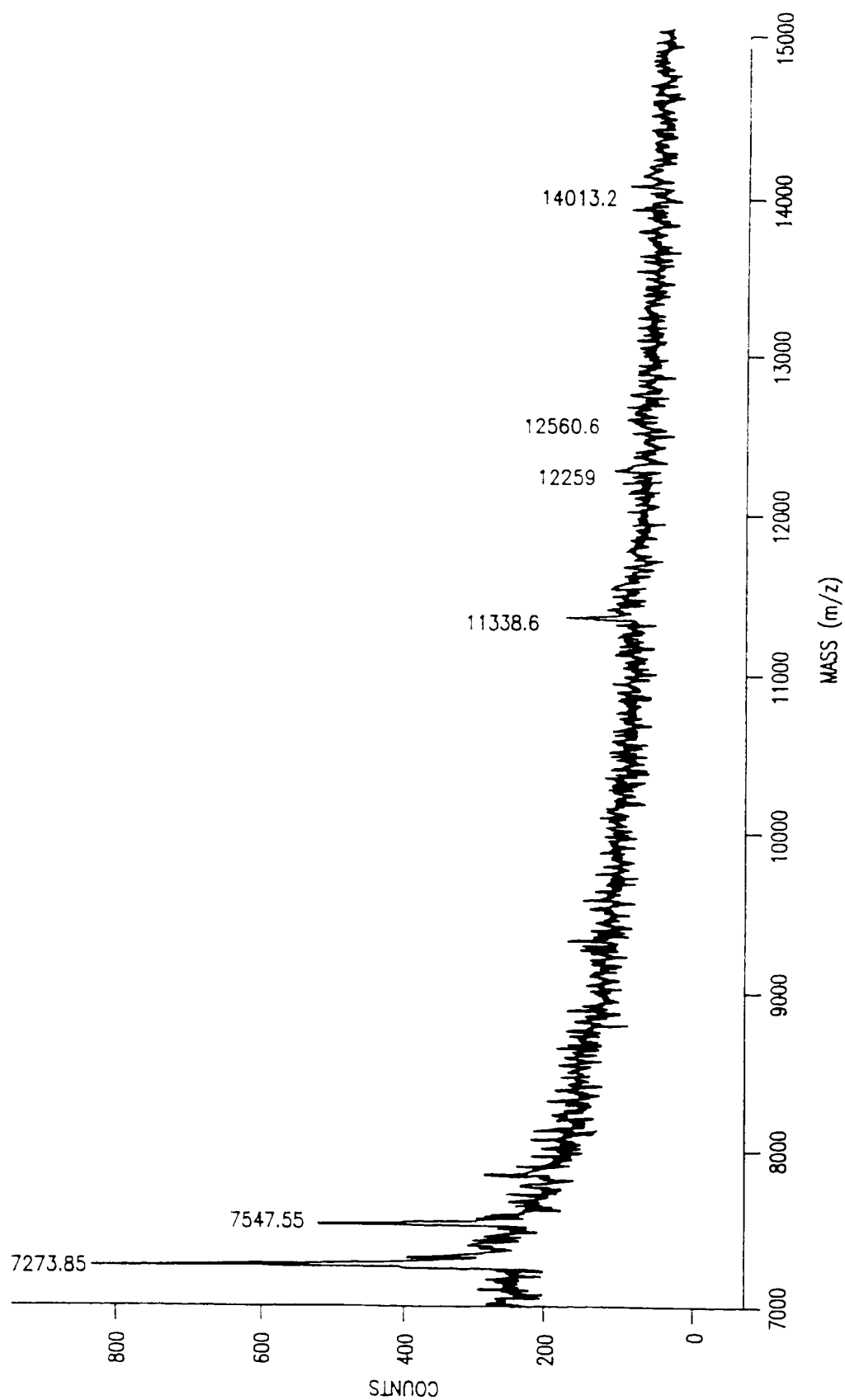


FIG. 86

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PCR PRODUCT
 CKR_Δ-F
 CAGCTCTCAT TTCCATACA GTCAGTATCA ATTCTGGAAG AATTCCAGACA TTAAAGAT
 AGTCATCTTG GGGCT GTCGAGAGTA AAAGGTATGT CAGTCATAGT TAAGACCTTC TTAAAGGTCT CKR_Δ-R-BIO
 GTAATTCTTA TCAGTAGAAC CCGGA-BIOTIN

FIG. 87A

SIZE ANALYSES: WILDTYPE
 SENSE STRAND W/O A:
 CAGCTCTCAT TTCCATACA GTCAGTATCA ATTCTGGAAG AATTCCAGACA CATTAAAGAT
 AGTCATCTTG GGGCT 75 bp 23036 Da
 SENSE STRAND WITH A:
 CAGCTCTCAT TTCCATACA GTCAGTATCA ATTCTGGAAG AATTCCAGACA CATTAAAGAT
 AGTCATCTTG GGGCTA 76 bp 23349 Da

FIG. 87B

SIZE ANALYSES: 32 bp DELETION
 SENSE STRAND W/O A:
 CAGCTCTCAT TTCCATACA TTAAAGAT AGTCATCTTG GGGCT 43 bp 13143 Da
 SENSE STRAND WITH A:
 CAGCTCTCAT TTCCATACA TTAAAGAT AGTCATCTTG GGGCTA 44 bp 13456 Da
 PROBE ANALYSES: WILDTYPE (ddITP TERMINATION):
 CAGCTCTCAT TTCCATACA GT 22 bp 6604 Da

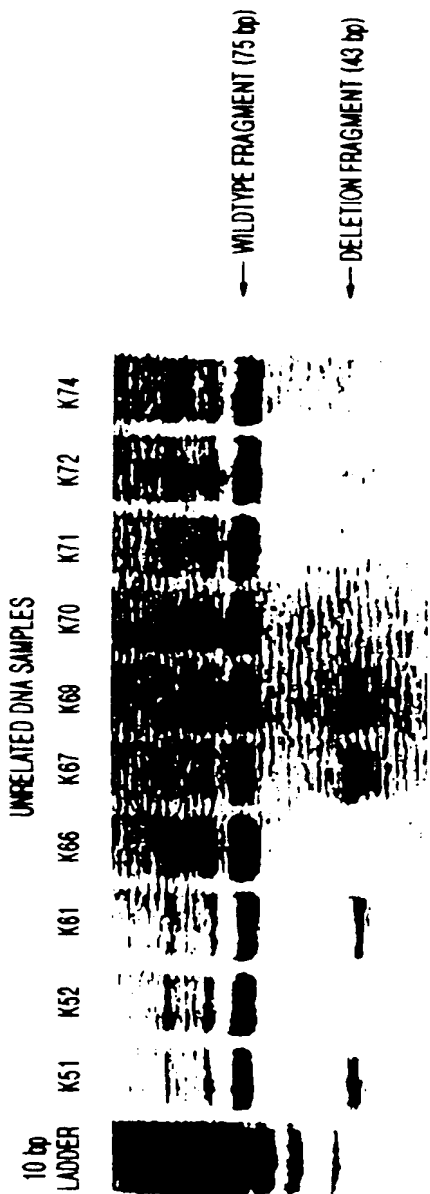
FIG. 87C

PROBE ANALYSES: 32 bp DELETION (ddITP TERMINATION):
 CAGCTCTCAT TTCCATACA T 21 bp 6275 Da

*FIG. 87D**FIG. 87E*

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DETECTION OF A 32 bp DELETION IN THE CHEMOKINE RECEPTOR BY PCR AND 15% NATIVE PAGE



DELETION FRAGMENTS ARE ONLY WEEKLY STAINED BY SILVER

FIG. 88

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HETEROZYGOUS

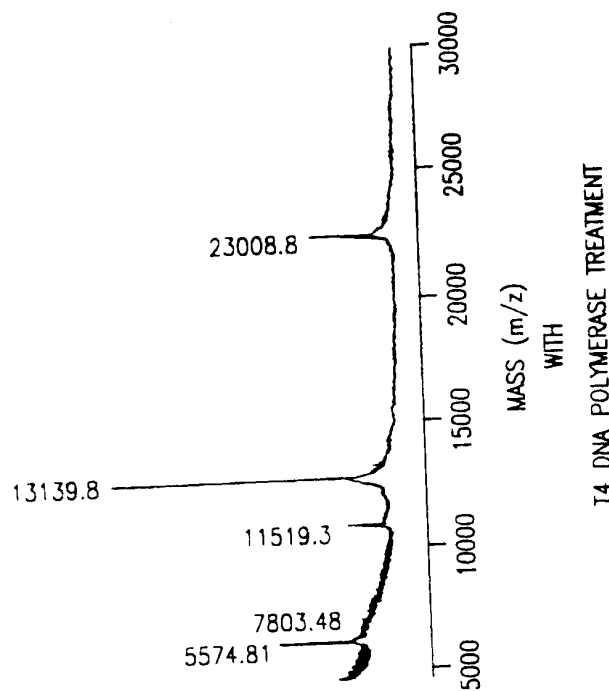


FIG. 89B

HETEROZYGOUS

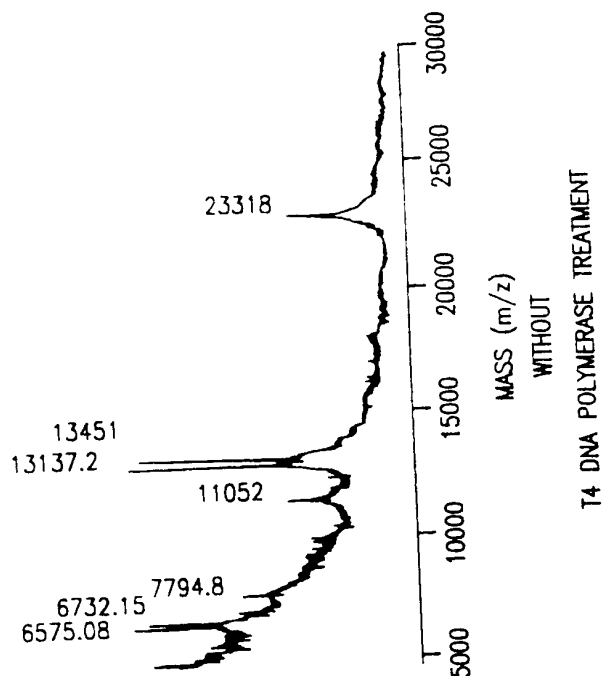


FIG. 89A

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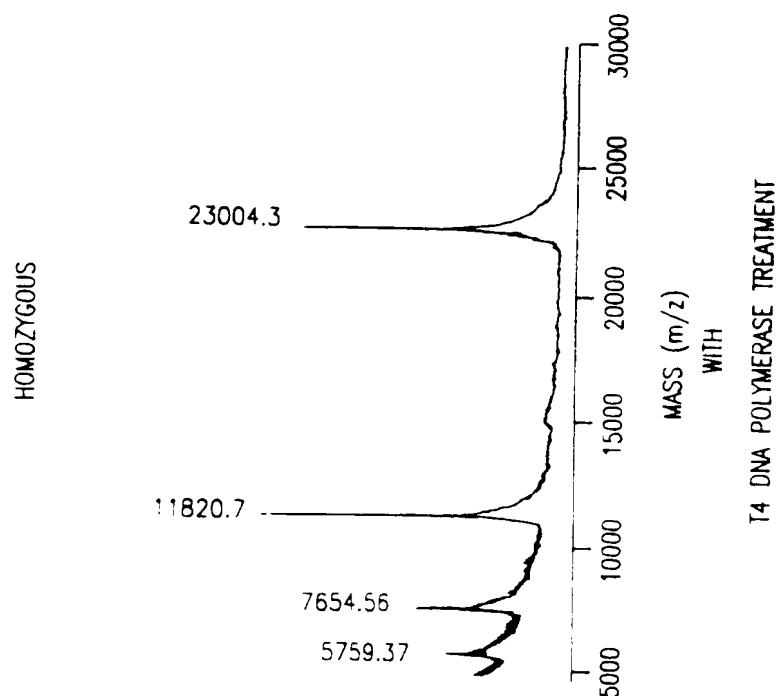


FIG. 89D

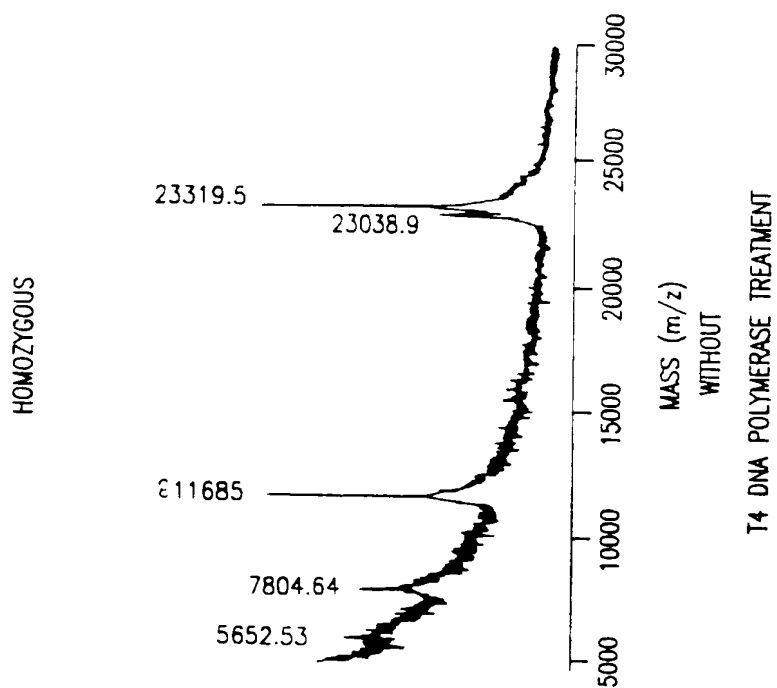


FIG. 89C

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FIG. 90A

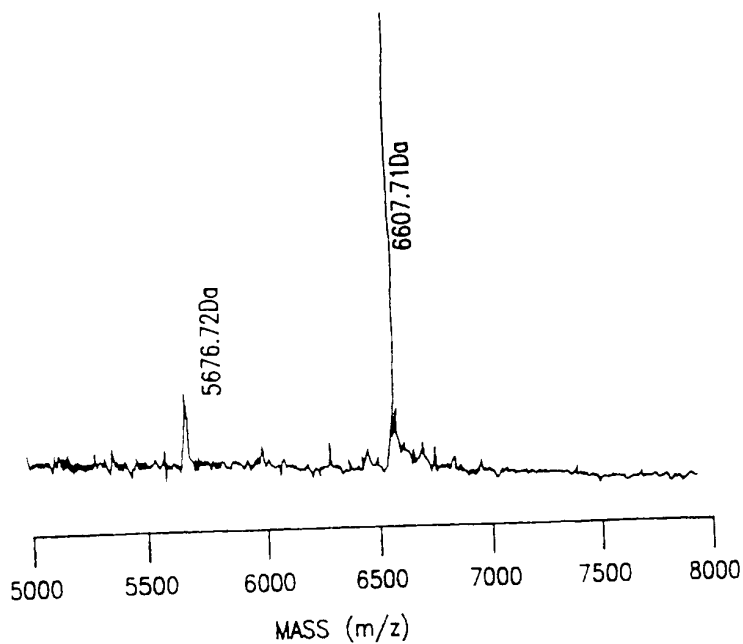
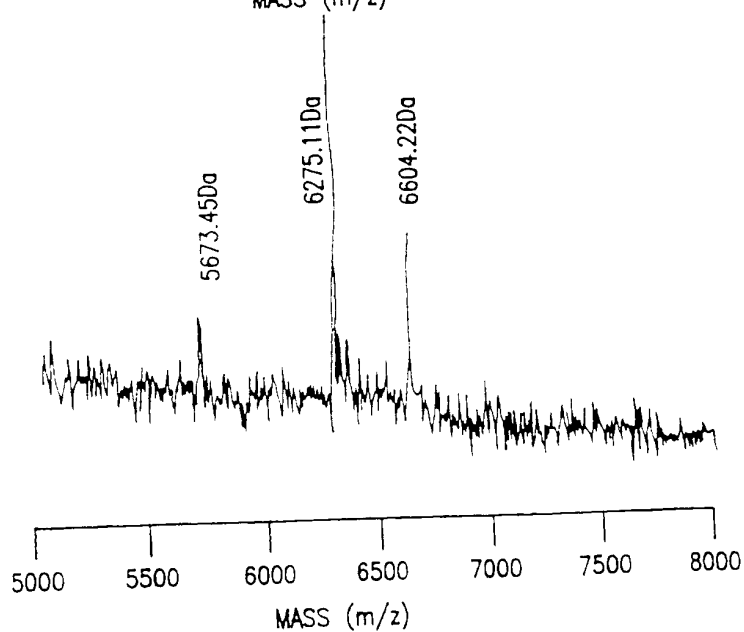


FIG. 90B



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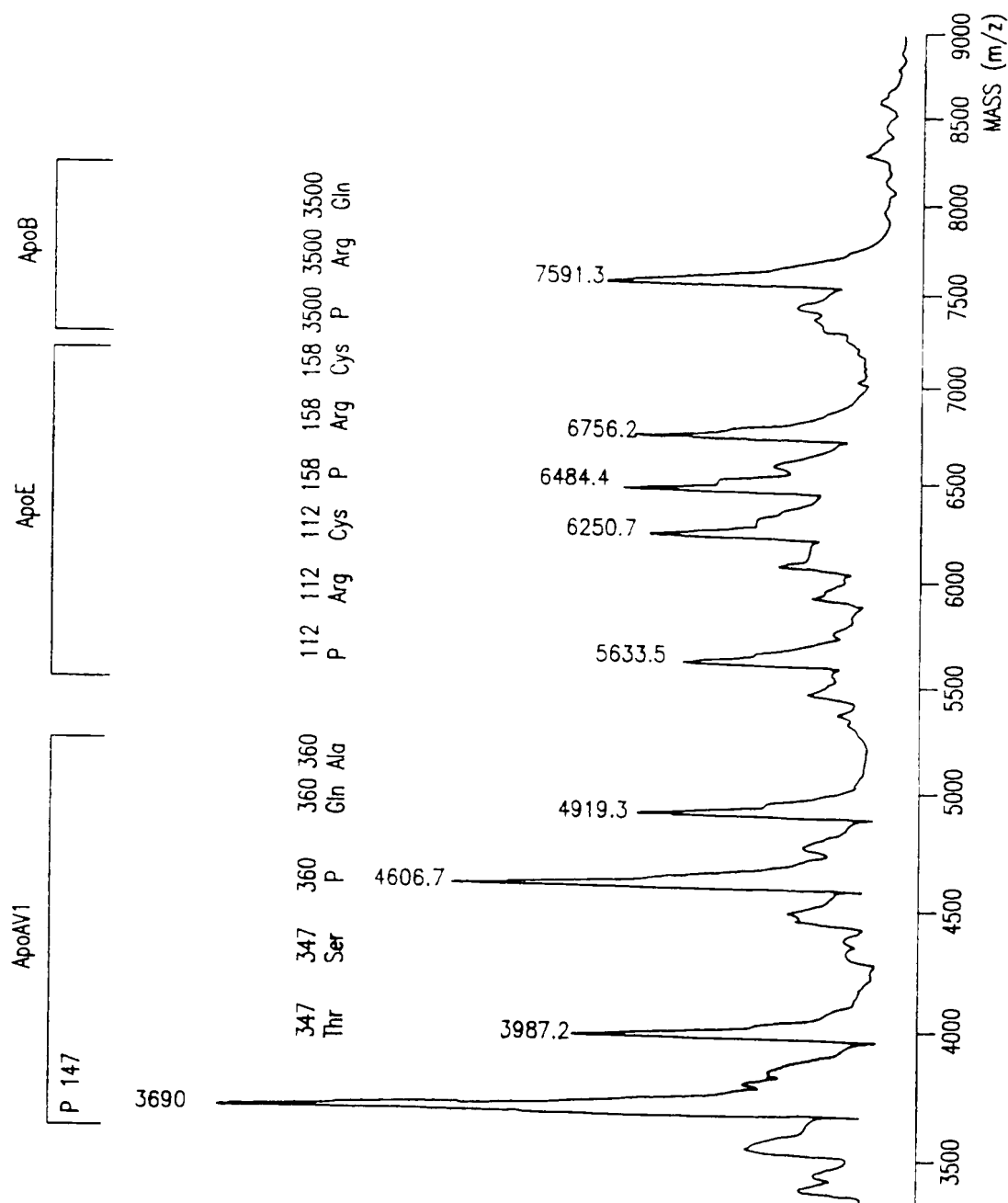


FIG. 91

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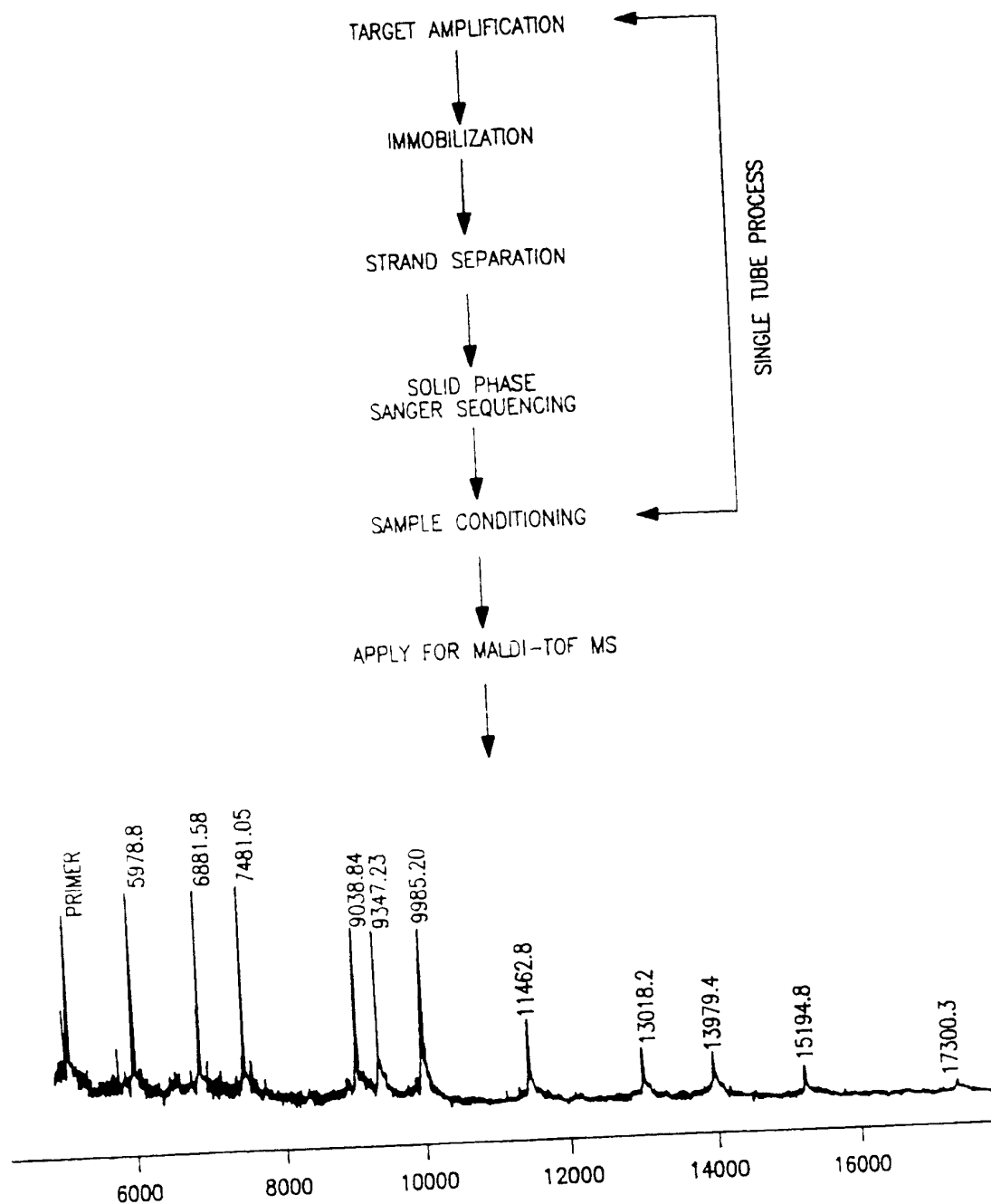


FIG. 92

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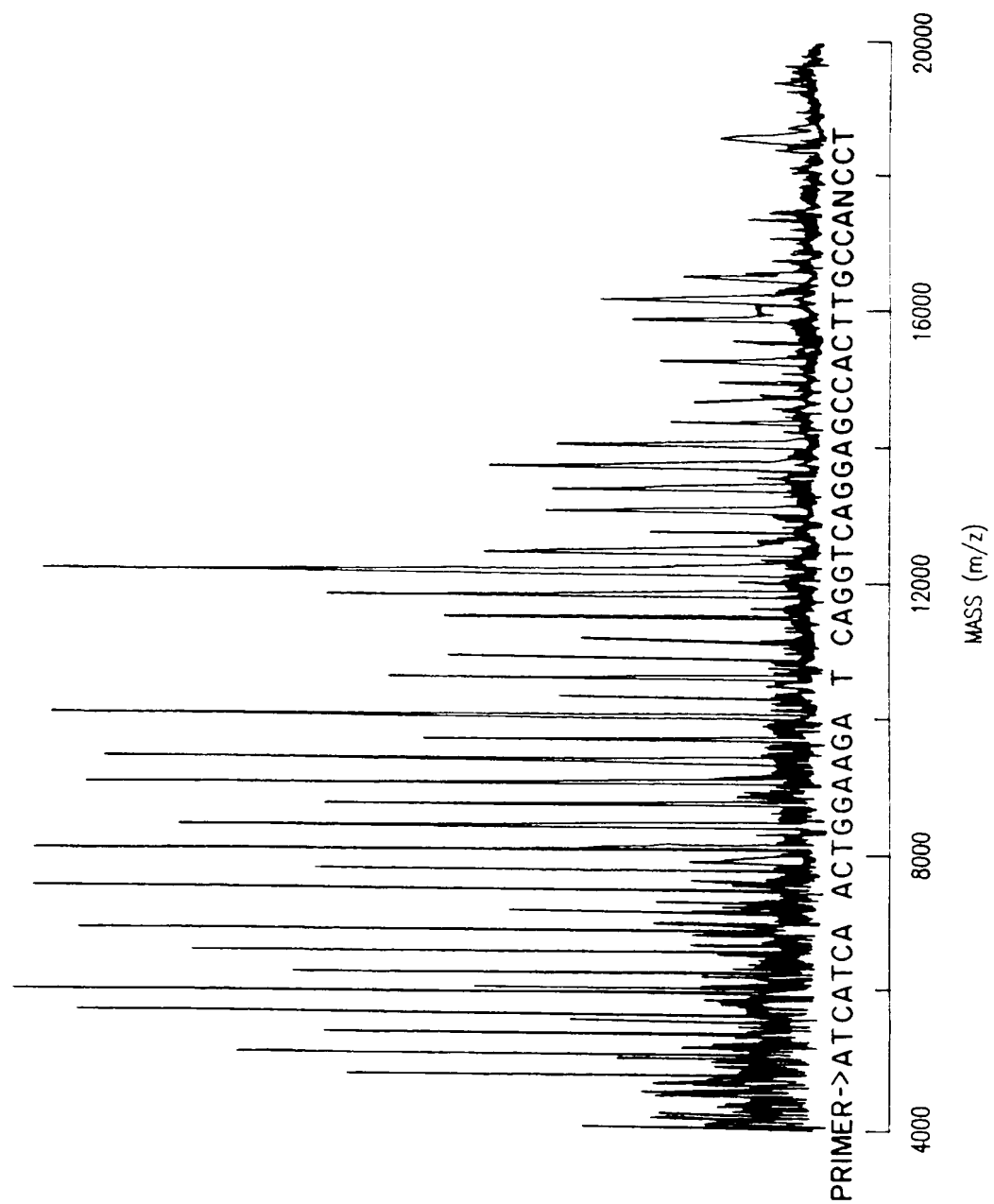
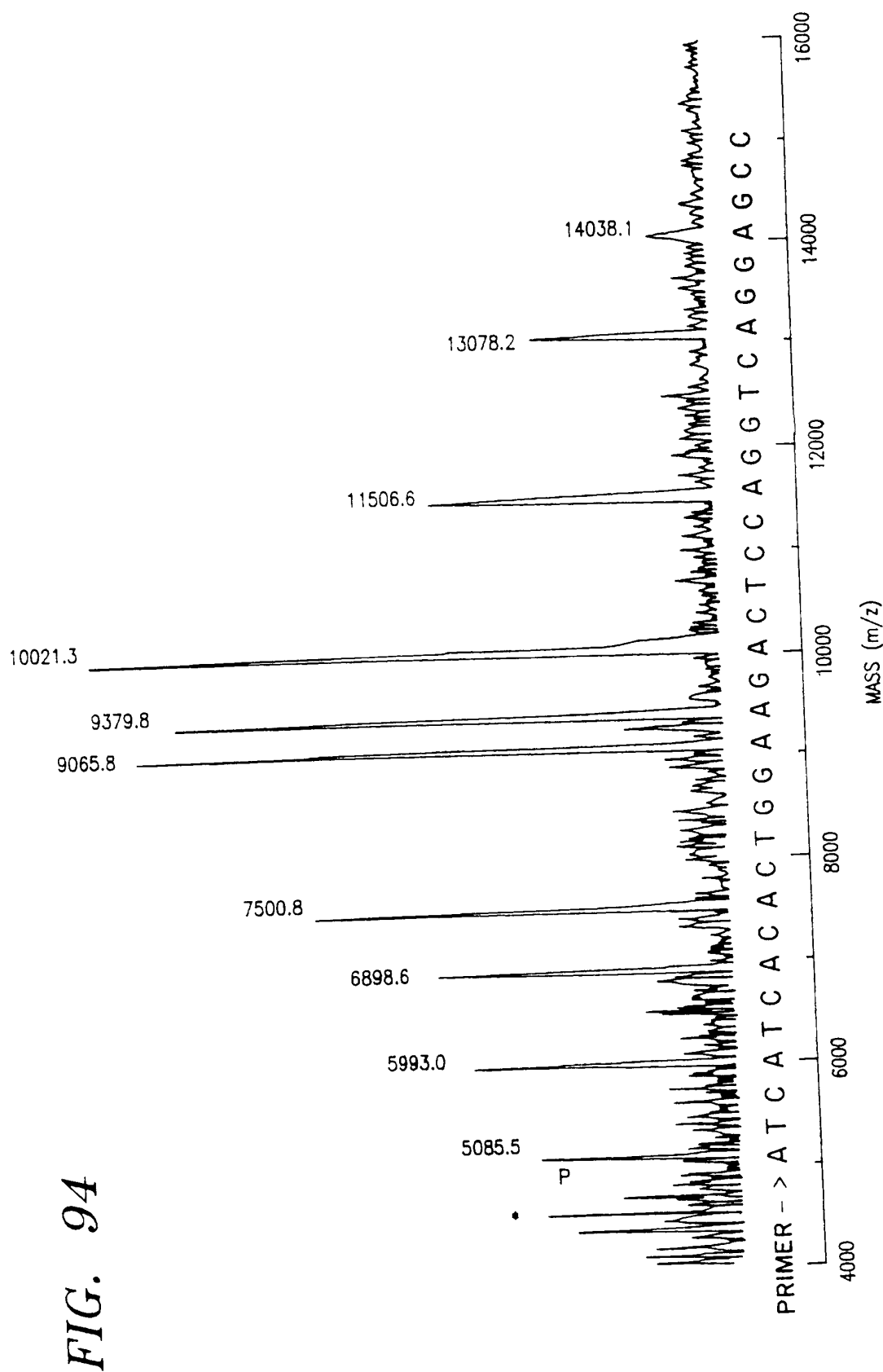


FIG. 93

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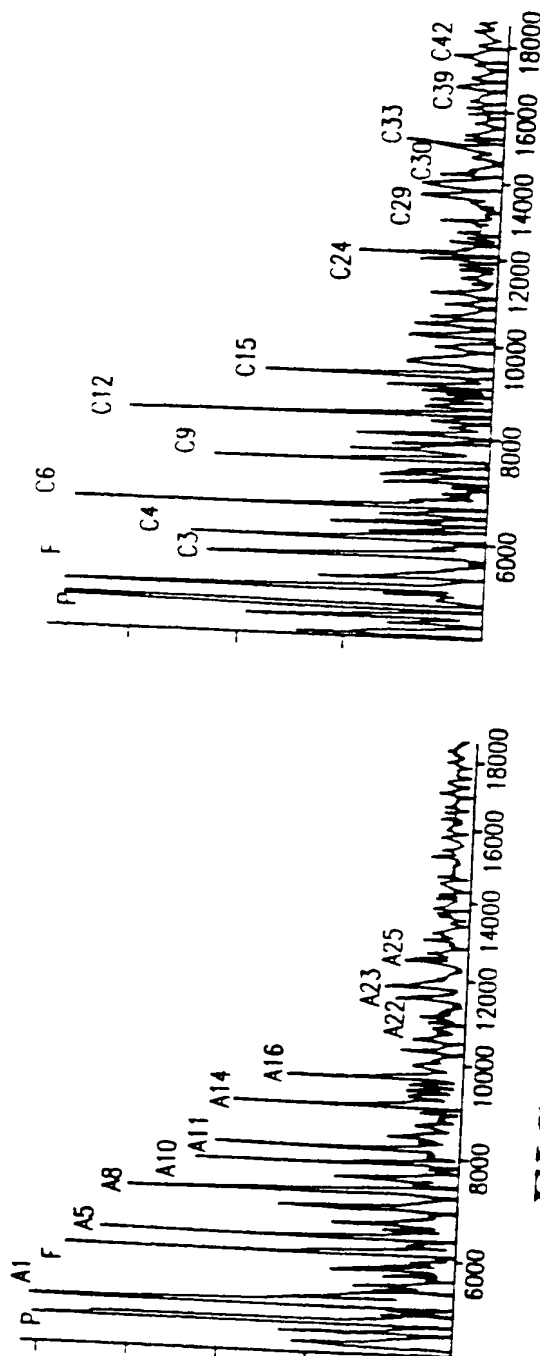


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1. MICROITER PLATE ISOTHERMAL SEQUENCING
2. 'PIEZOELECTRIC PIPETTE' TRANSFER
3. CORETECH MS

P-AICCACTACACTACATGCTGTAACAGTTGG*GCG*GdGdCddC
 5 10 15 20 25 30 35 40



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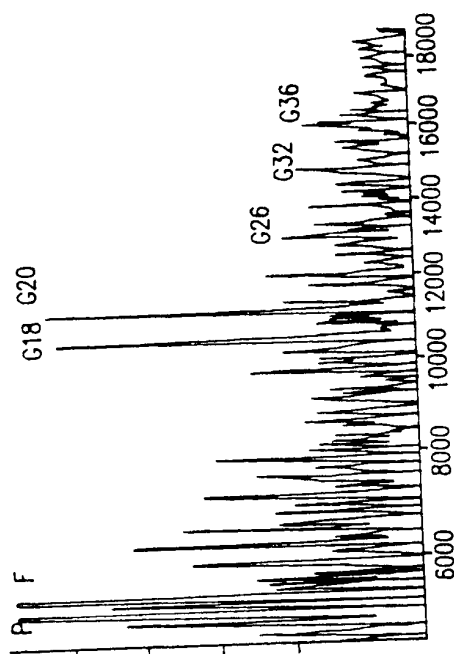


FIG. 95D

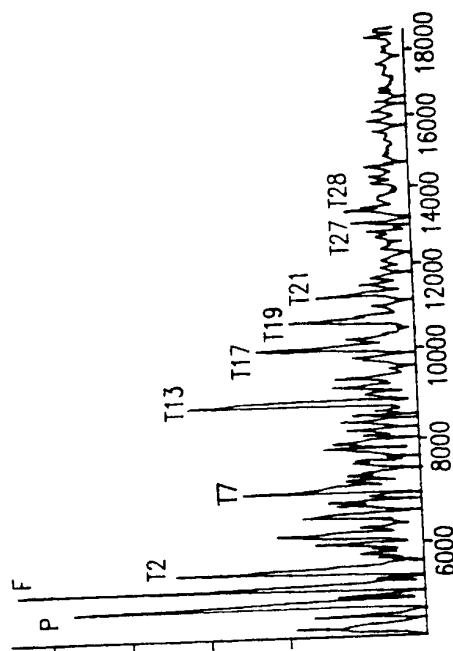


FIG. 95C

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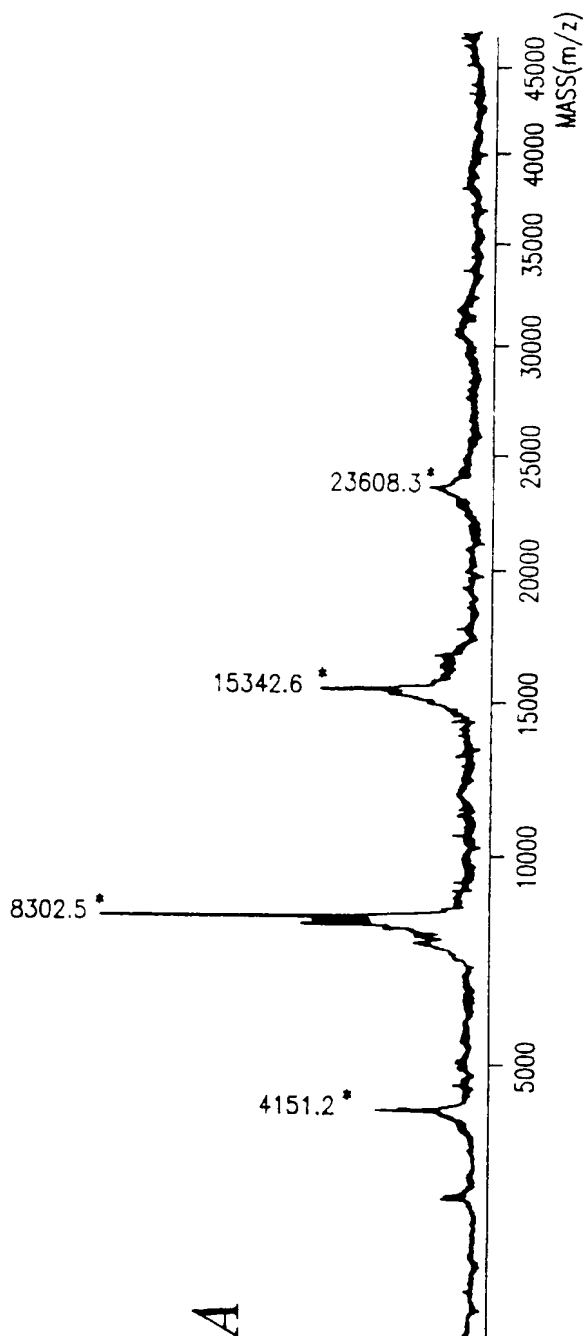


FIG. 96A

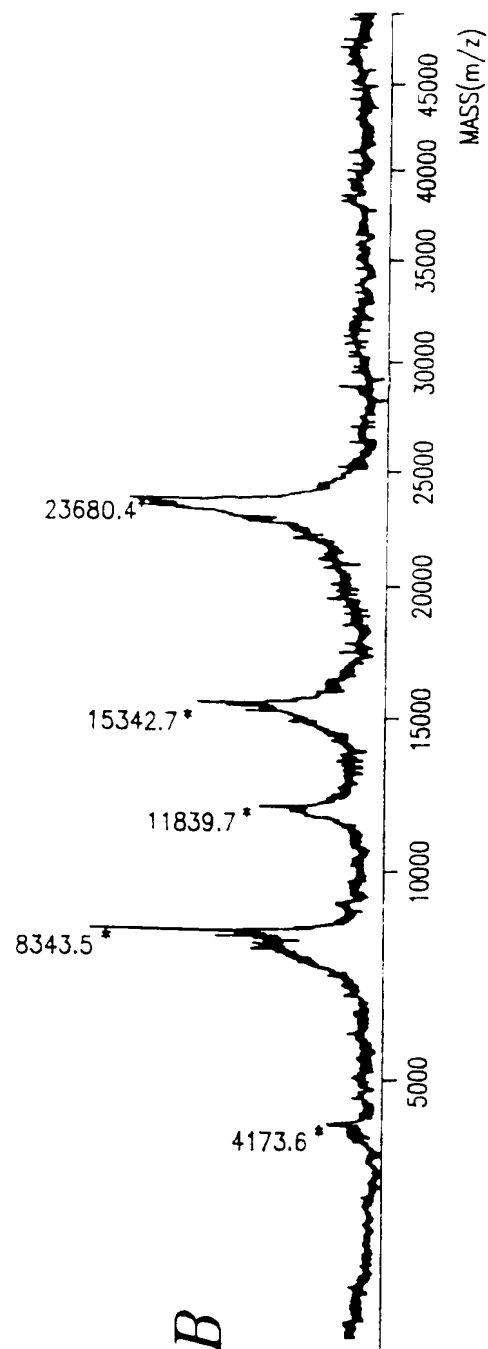


FIG. 96B

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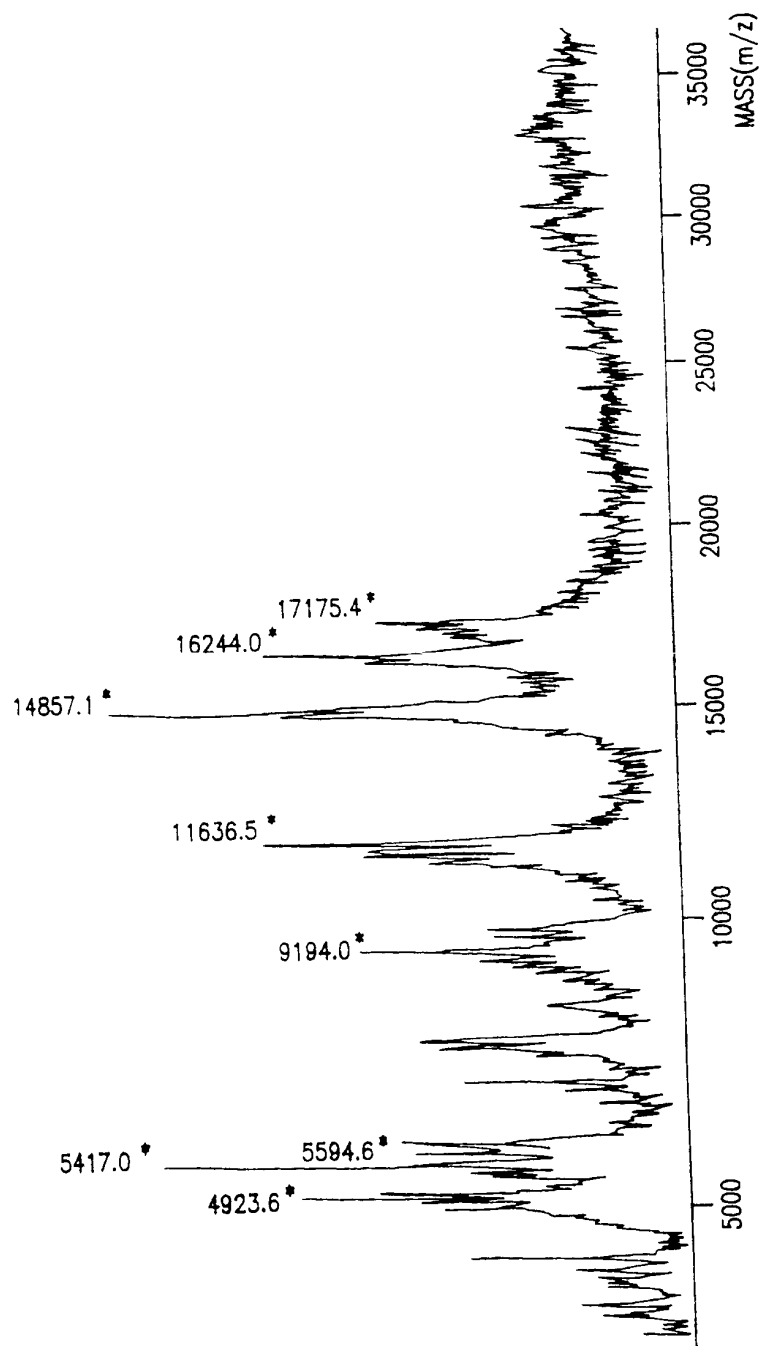


FIG. 97A

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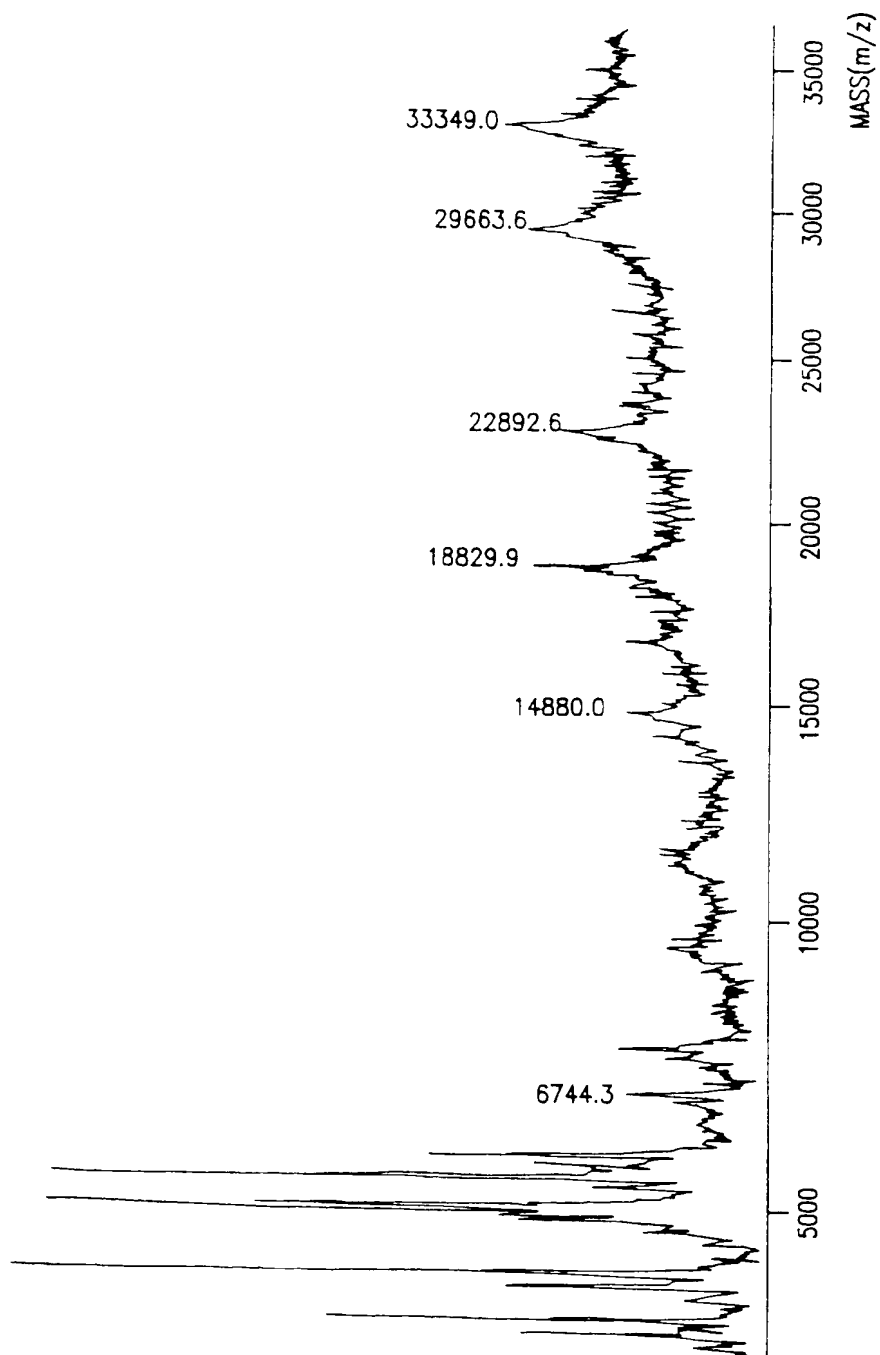


FIG. 97B

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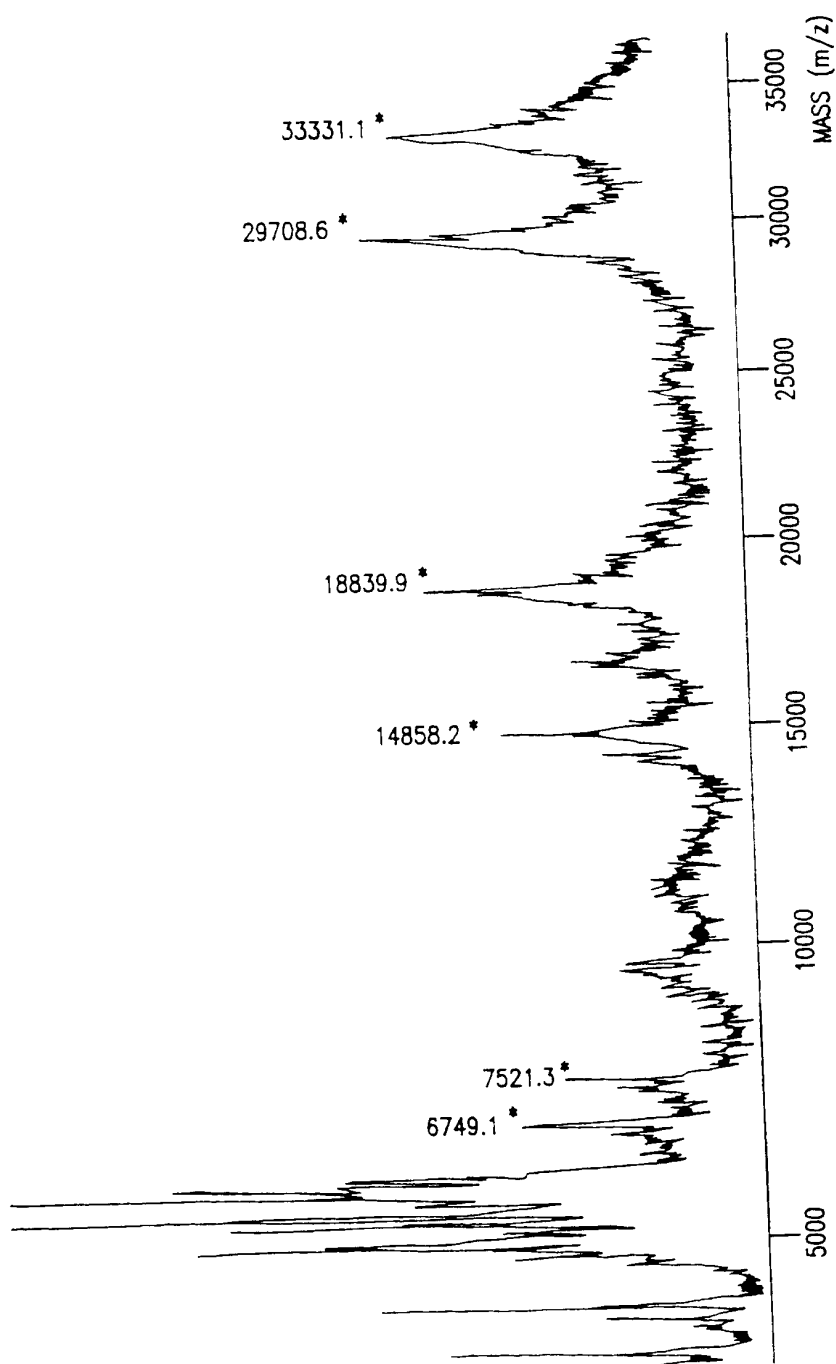


FIG. 98

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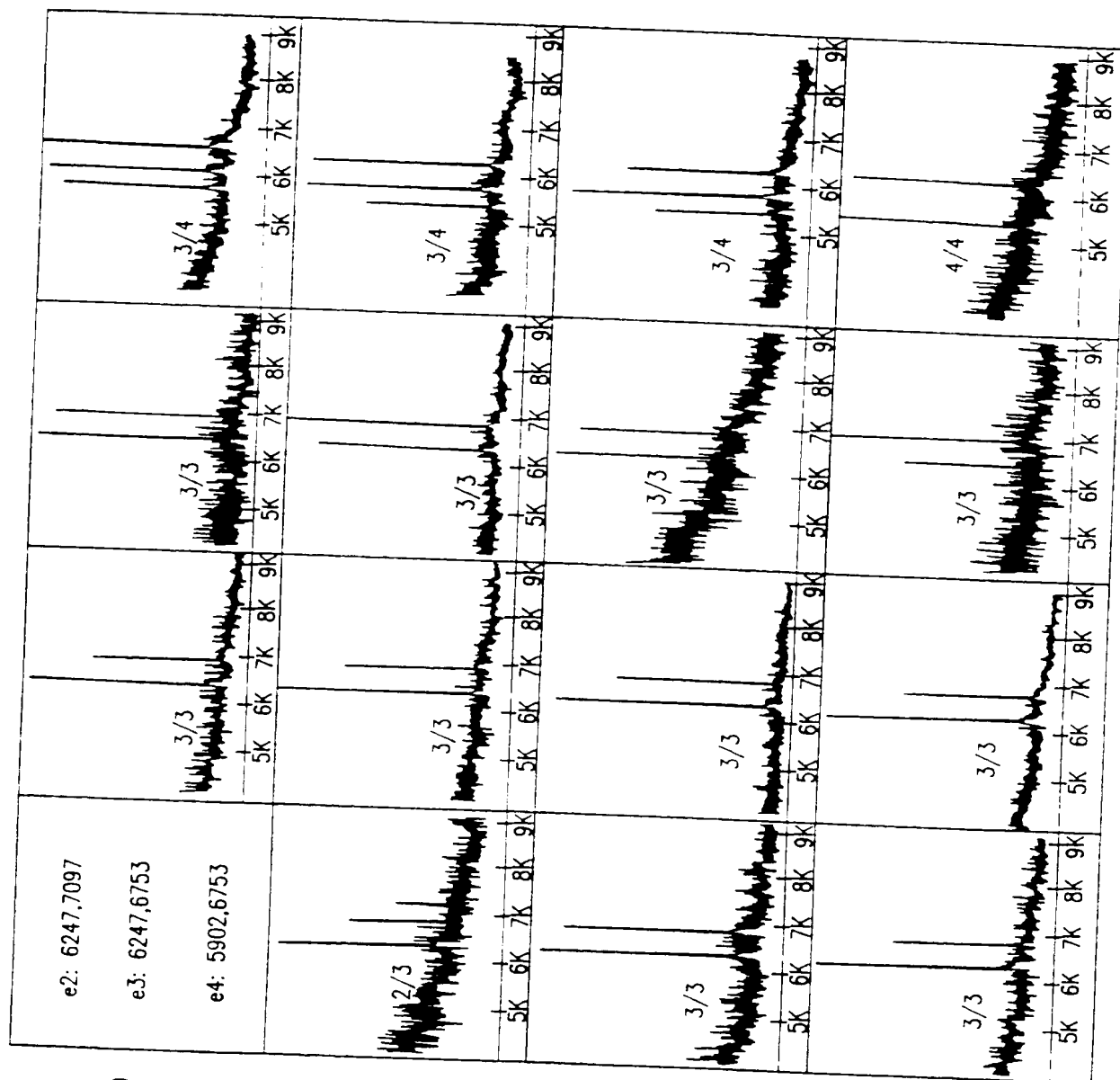


FIG. 99

Apo E
 CODONS 112&158
 • ISOTHERMAL PROBE
 • PIN TRANSFER (~10nL)
 • MALDI-MS

70% EXPECTED
 ALLELIC FREQUENCY

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1-20: 5'-GUC ACU ACA GGU GAG CUC CA-3'

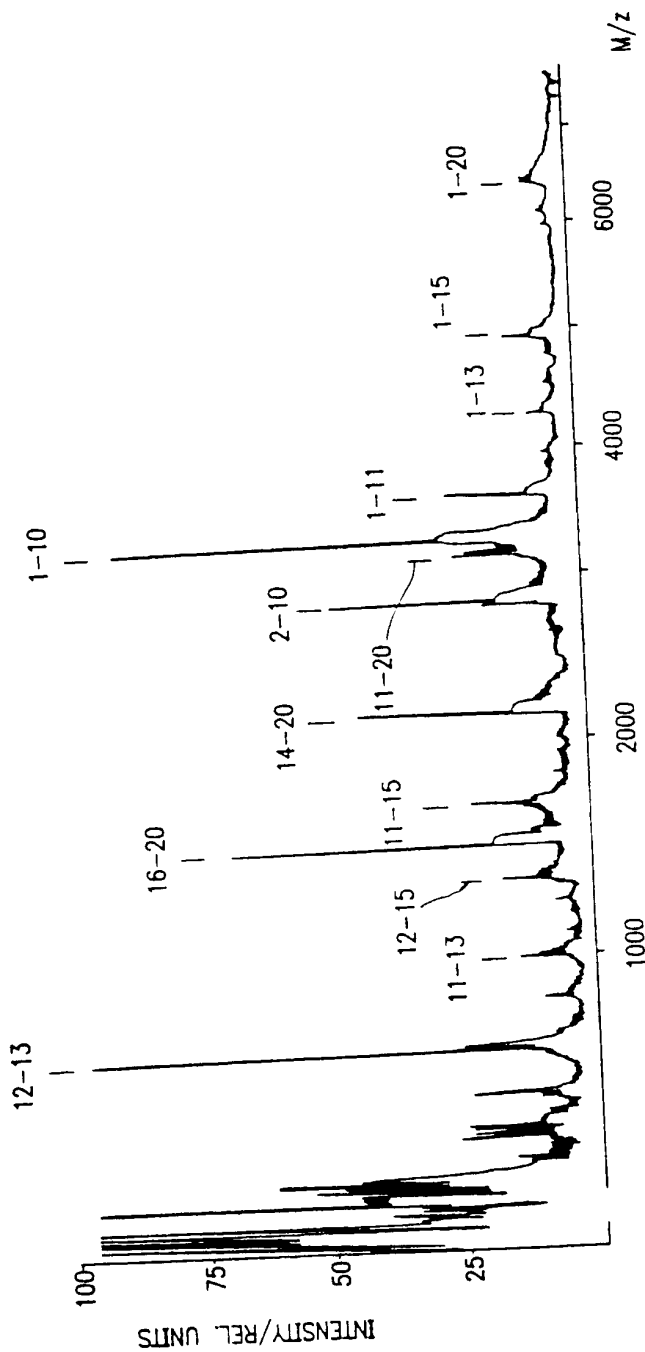


FIG. 100



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International Bureau



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : C12Q 1/68, C07H 21/00, C07F 9/24		A3	(11) International Publication Number: WO 98/20166																								
(21) International Application Number: PCT/US97/20444		(43) International Publication Date: 14 May 1998 (14.05.98)																									
(22) International Filing Date: 6 November 1997 (06.11.97)		(74) Agent: SEIDMAN, Stephanie, L.; Brown Martin Haller & McClain, 1660 Union Street, San Diego, CA 92101-2926 (US).																									
(30) Priority Data: <table border="0"><tr><td>08/744,481</td><td>6 November 1996 (06.11.96)</td><td>US</td></tr><tr><td>08/746,036</td><td>6 November 1996 (06.11.96)</td><td>US</td></tr><tr><td>08/746,055</td><td>6 November 1996 (06.11.96)</td><td>US</td></tr><tr><td>08/744,590</td><td>6 November 1996 (06.11.96)</td><td>US</td></tr><tr><td>08/786,988</td><td>23 January 1997 (23.01.97)</td><td>US</td></tr><tr><td>08/787,639</td><td>23 January 1997 (23.01.97)</td><td>US</td></tr><tr><td>08/933,792</td><td>19 September 1997 (19.09.97)</td><td>US</td></tr><tr><td>08/947,801</td><td>8 October 1997 (08.10.97)</td><td>US</td></tr></table>		08/744,481	6 November 1996 (06.11.96)	US	08/746,036	6 November 1996 (06.11.96)	US	08/746,055	6 November 1996 (06.11.96)	US	08/744,590	6 November 1996 (06.11.96)	US	08/786,988	23 January 1997 (23.01.97)	US	08/787,639	23 January 1997 (23.01.97)	US	08/933,792	19 September 1997 (19.09.97)	US	08/947,801	8 October 1997 (08.10.97)	US	(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).	
08/744,481	6 November 1996 (06.11.96)	US																									
08/746,036	6 November 1996 (06.11.96)	US																									
08/746,055	6 November 1996 (06.11.96)	US																									
08/744,590	6 November 1996 (06.11.96)	US																									
08/786,988	23 January 1997 (23.01.97)	US																									
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08/933,792	19 September 1997 (19.09.97)	US																									
08/947,801	8 October 1997 (08.10.97)	US																									
(71) Applicant (for all designated States except US): SEQUENOM, INC. [US/US]; 11555 Sorrento Valley Road, San Diego, CA 92121 (US).		Published <i>With international search report. Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i>																									
(72) Inventors; and		(88) Date of publication of the international search report: 22 October 1998 (22.10.98)																									
(75) Inventors/Applicants (for US only): KOSTER, Hubert [DE/US]; 8636 C Via Mallorca Drive, La Jolla, CA 92037 (US). TANG, Kai [CN/US]; 8521 Summerdale Road #241, San Diego, CA 92126 (US). FU, Dong-Jing [CN/US]; 10615 Dabney Drive #21, San Diego, CA 92126 (US). SIEGERT, Carston, W. [DE/US]; Geielstrasse 42, D-22303 Hamburg (DE). LITTLE, Daniel, P. [US/US]; 393 Glendale Lake Road, Patton, PA 18668 (US). HIGGINS, G., Scott [GB/DE]; Haselweg 1, D-22880 Weidel (DE). BRAUN, Andreas [DE/US]; 13232 Benchley Road, San Diego, CA 92130 (US). DAMHOFFER-DEMAR, Brigitte																											
(54) Title: DNA DIAGNOSTICS BASED ON MASS SPECTROMETRY																											
(57) Abstract <p>Fast and highly accurate mass spectrometry-based processes for detecting a particular nucleic acid sequence in a biological sample are provided. Depending on the sequence to be detected, the processes can be used, for example, to diagnose a genetic disease or chromosomal abnormality; a predisposition to a disease or condition, infection by a pathogenic organism, or for determining identity or heredity.</p>																											

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INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 97/20444

A. CLASSIFICATION OF SUBJECT MATTER
IPC 6 C12Q1/68 C07H21/00 C07F9/24

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Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

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Date of the actual completion of the international search

29 July 1998

Date of mailing of the international search report

28.08.98

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Osborne, H

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Patent Application No.

PCT/US 97/20444

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X	WO 96 29431 A (SEQUENOM INC) 26 September 1996	1
X	pages 25-54	2-7,
	see page 9, line 33 - page 10, line 2;	11-18,
	claims 1-49; figure 9	82,83
X	see page 15, line 34 - page 18, line 10;	19-34,
	examples 5,8	82,83
X	see example 8	42
X	see page 16, line 4; figures 6A,8	47
X	page 36, ln 33	48,49,
	see page 26, line 7	80,81
X	see page 16 - page 18, line 10; figures 3-9	50-64,
		68-70
Y	see page 21, line 21 - line 23	35-37
Y	see example 7	38,39
Y	see claims 1-49	40,41,
		43-47,
		65-67,
		71-79

Y	WO 94 16101 A (KOESTER HUBERT) 21 July 1994	1-7,
		11-18,
		65-79,
		82,83
	see the whole document	

Y	WO 96 32504 A (UNIV BOSTON) 17 October 1996	1-7,
		11-18,
		66-79,
		82,83
	especially page 21, lns 12-24.	
	see the whole document	

Y	WO 95 13381 A (GERON CORP) 18 May 1995	35-37,
		82,83
	see page 9, line 1 - line 33	
	see page 29, line 34 - page 32, line 5	
	see claims 1-4; example 3	

Y	FENG J ET AL: "THE RNA COMPONENT OF HUMAN TELOMERASE"	35-37,
	SCIENCE,	82,83
	vol. 269, no. 5228, 1 September 1995,	
	pages 1236-1241, XP000645335	
	see page 1236, paragraph 1 - paragraph 4	

Y	SYVANEN A -C ET AL: "DETECTION OF POINT MUTATIONS BY SOLID-PHASE METHODS"	35,38,
	HUMAN MUTATION,	39,82,83
	vol. 3, no. 3, 1 January 1994, pages 172-179, XP000600258	
	see the whole document	

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 International Application No
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Y	PASINI B ET AL: "RET mutations in human disease" TRENDS IN GENETICS, vol. 12, no. 4, April 1996, pages 138-144, XP002072975 see page 141, paragraph 2 - page 144 ---	35,38, 39,82,83
Y	DE 44 31 174 A (DEUTSCHES KREBSFORSCH) 7 March 1996 see abstract and claim 1 ---	40,41
Y	NAITO H ET AL: "Detection of tyrosine hydroxylase mRNA and minimal Neuroblastoma cells by reverse transcription-polymerase chain reaction " EUROPEAN JOURNAL OF CANCER, vol. 27, June 1991, pages 762-65, XP002073102 see the whole document ---	40,41
Y	GB 2 260 811 A (YORKSHIRE CANCER RESEARCH CAMP ;UNIV LEEDS (GB)) 28 April 1993 see the whole document ---	40,41
Y	WO 96 17080 A (IMP CANCER RES TECH ;SELBY PETER JOHN (GB); BURCHILL SUSAN ANN (GB) 6 June 1996 see page 3, line 1 - line 2 ---	35,40, 41,82,83
Y	NELSON R ET AL: "Time-of-flight Mass spectrometry of nucleic acids by laser ablation and ionization from a frozen aqueous matrix " RAPID COMMUNICATIONS IN MASS SPECTROMETRY, vol. 4, September 1990, pages 348-351, XP002072976 see abstract ---	42,82,83
Y	TANG K ET AL: "MATRIX-ASSISTED LASER DESORPTION/IONIZATION OF RESTRICTION ENZYME-DIGESTED DNA" RAPID COMMUNICATIONS IN MASS SPECTROMETRY, vol. 8, no. 2, February 1994, pages 183-186, XP000608266 see the whole document ---	42,82,83
Y	SIEGERT C ET AL: "Matrix-assisted laser desorption/ionization Time-of-flight Mass Spectrometry for the detection of polymerase chain reaction products containing 7-Deazapurine moieties" ANALYTICAL BIOCHEMISTRY, vol. 243, 1996, pages 55-65, XP002072977 see the whole document ---	42,82,83

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Patent Application No.

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C. (Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	WO 95 15400 A (UNIV JOHNS HOPKINS) 8 June 1995 see abstract and claims 1-19 ---	43-45, 82,83
Y	WO 96 10648 A (PROMEGA CORP) 11 April 1996 see claims 1,23 ---	43-45, 82,83
Y	WO 93 23563 A (CEMU BIOTEKNIK AB ;UHLEN MATHIAS (SE); PETTERSSON BERTIL (SE)) 25 November 1993 see claims 1-7; figure 1 ---	46,82,83
Y	DE 44 38 630 A (PACHMANN KATHARINA DR ;GOEHL URSULA (DE)) 2 May 1996 see claim 1; figures 1A,1B ---	46,82,83
Y	EP 0 593 789 A (SUMITOMO METAL IND) 27 April 1994 see abstract, claims 1 and 2 ---	46,82,83
Y	WO 96 15262 A (MEDINNOVA SF ;DZIEGLEWSKA HANNA EVA (GB); BREIVIK JARLE (NO); GAUD) 23 May 1996 see page 12, paragraph 4 - page 13, paragraph 2 ---	46,82,83
Y	WO 89 06700 A (GENENTECH INC) 27 July 1989 see the whole document ---	47,82,83
Y	WO 89 03432 A (US ENERGY) 20 April 1989 see claims 1-21; figures 1,2 ---	65,68-70
Y	US 5 288 644 A (BEAVIS RONALD C ET AL) 22 February 1994 see claims 1-8 ---	66,67
X	WO 94 21822 A (KOESTER HUBERT) 29 September 1994 see claims 1-55 ---	65-79
X	US 5 430 136 A (URDEA MICHAEL S ET AL) 4 July 1995 see column 4, line 28 - column 9, line 52 ---	84-87
X	WO 95 31429 A (UNIV BOSTON) 23 November 1995 see claims 1,19 ---	84-87

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INTERNATIONAL SEARCH REPORT

nal Application No

PCT/US 97/20444

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	ORDOUKHANIAN P ET AL: "Design and synthesis of a versatile photocleavable DNA building block. application to phototriggered hybridization" JOURNAL OF THE AMERICAN CHEMICAL SOCIETY, vol. 117, 1995, pages 9570-71, XP002072978 see the whole document ---	84-87
E	WO 97 42348 A (SEQUENOM INC) 13 November 1997 see claims 1-48 -----	1,7-10

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 97/20444

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

- 1 ☐ Claims Nos. _____
because they relate to subject matter not required to be searched by this Authority, namely _____
- 2 ☐ Claims Nos. _____
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically _____
- 3 ☐ Claims Nos. _____
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a)

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

SEE ANNEXES

- 1 ☒ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
- 2 ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
- 3 ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos. _____
- 4 ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos. _____

Remark on Protest

- ☒ The additional search fees were accompanied by the applicant's protest
- ☐ No protest accompanied the payment of additional search fees

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

It should be further noted that "claims 82-83" as designated herein refer to two claims 82 and two claims 83 which were filed as follows, claims 82, 83 followed by a second claim 82 and a second claim 83)

1. Claims 1-18, partially 82-83:

A method for determining the sequence of a target nucleic acid involving the generation of base specifically terminated fragments.

2. Claims 19-34, partially 82-83:

A method for detecting a target nucleic acid present in a biological sample based on a nested polymerase chain amplification reaction.

3. Claim 35 partially (in that it relates to the detection of neoplasia/malignancies by detecting telomerase), claims 36 and 37, and partially 82-83:

An assay for the detection of neoplasia/malignancies based on telomerase specific extension of a substrate primer and a subsequent amplification of the telomerase specific extension product by PCR.

4. Claim 35 partially (in that it relates to the detection of neoplasia/malignancies by detecting mutation of a proto-oncogene), claims 38 and 39, and partially claims 82-83:

An assay for the detection of neoplasia involving mutation analysis of mutant or wild-type alleles by primer extension reaction by a Sanger type sequencing protocol.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

6. Claim 18 partially in that it relates to the detection of neoplasia/malignancies by detecting expression of a tumour-specific gene in a specific tissue type), claims 40 and 41, and partially claims 32-33:

An amplification based assay for the expression of the tyrosine hydroxylase gene in bone marrow cells as indicative of a neuroblastoma.

7. Claim 21, partially claims 32-33:

A method for directly detecting double stranded nucleic acids using Matrix-Assisted Laser Desorption/Ionization (MALDI-TOF) mass spectrometry.

8. Claims 22-24, partially claims 32-33:

A method for comparing DNA relatedness by amplification of microsatellite DNA repeat sequences.

9. Claim 25, partially claims 32-33:

A method for detecting mutations based on target amplification using a primer that introduces a unique endonuclease restriction site into amplified target and a combination of a Sanger sequencing protocol and endonuclease digestion.

10. Claim 47, partially claims 32-33:

A method for the amplification and detection of a nucleic acid based on the synthesis of RNA using a primer containing a RNA polymerase promoter sequence.

11. Claims 48, 49, 50 and 51, partially 32-33:

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Primers per se for mass spectrometry comprising a mass modifying moiety.

11. Claims 60-64, partially 68-70, partially 73-79, partially claims 82-83:

Method for detecting a target nucleic acid sequence involving hybridisation to a detector oligonucleotide.

12. Claims 65-67, partially 68-70, 71-72, partially 73-79, partially claims 82-83:

Means for determining a nucleic acid sequence involving exonuclease digestion.

13. Claims 84-94:

Photolabile linkers per se for use in immobilisation of nucleic acids to solid supports.

INTERNATIONAL SEARCH REPORT

Information on patent family members

Patent Application No

PCT/US 97/20444

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(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GATGCCGATG ACCTGCAGAA G

21

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GATGCCGATG ACCTGCAGAA GC

22

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

GATGCCGATG ACCTGCAGAA GTG

23

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:

-270-

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GTGCCCTGCA GCTTCACTGA AGAC

24

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GTGCCCTGCA GCTTCACTGA AGACTG

26

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GTGCCCTGCA GCTTCACTGA AGACC

25

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TATGTGTTCA CTGTGCCC

19

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(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

CAGAGGCCTG GGGACCCCTG

19

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

ACGACAGGGT TGETTGCC

18

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

ACTGACAACC ACCCTTAAC

19

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid

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(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

CTGCTTGCCA CAGGTCTC

18

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

CACAGCAGGC CAGTGTCT

18

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

GGACCTGATT TCCTTACTG

19

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

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(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

TGAATCTGAG GCATAACTG

19

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

TTGCGTACAC ACTGGCCGTC GTTTTACAAC GTCGTGACTG GGAAAACCCCT

50

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GTAAAACGAC GGCCAGTGTG TACGCAA

27

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

-274-

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

TACTGGAAGG CGATCTCAGC AATCAGC

27

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

GGCACGGCTG TCCAAGGAG

19

(189) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

AGGCCGCGCT CGGCGCCCTC

20

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: RNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

GUCACUACAG GUGAGCUCCA

20

(2) INFORMATION FOR SEQ ID NO:115:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GAATTCGAGC TCGGTACCCG G

21

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

CCGGGTACCG AGCTCGAATT C

21

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

CCTCTTGGGA ACTGTGTAGT ATT

23

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

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- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

AGGCTGTCTC TCTCCTCTC TCATACACAC ACACACACAC ACACACACAC ACACACACAC 60
ACACACACAC TCACACTCAC CCACANNNA ATACTACACA GTTCCCAAGA GG 112

(2) INFORMATION FOR SEQ ID NO:119:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 49 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

TAATACGACT CACTATAGGG CGAAGGCTGT CTCTCTCCCT CTCTCATAC 49

(2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 135 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

TAATACGACT CACTATAGGG CGAAGGCTGT CTCTCTCCCT CTCTCATACA CACACACACA 60
CACACACACA CACACACACA CACTCACACT CACCCACANN NAAATACTAC 120
ACAGTTCCCA AGAGG 135

(2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

-277-

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

AATACTACAC AG

12

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

CTGATGCGTC GGATCATCTT TTTT

24

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

GATGATCCGA CGCATCAGAA TGT

23

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

GATCTAGCTG GGCCGAGCTA GGCCGTTGA

29

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

-278-

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

CTGATGCGTC GGATCATCTT TTTTTTT

27

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

GATGATCCGA CG

12

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

GATGATCCGA CGCAT

15

(2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO

-279-

(iv) ANTISENSE: NO
 (v) FRAGMENT TYPE:
 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

AAAAAAGATG AT

12

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 12 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTISENSE: NO
 (v) FRAGMENT TYPE:
 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

GATCCGACGC AT

12

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 253 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTISENSE: NO
 (v) FRAGMENT TYPE:
 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

GGCACGGCTG	TCCAAGGAGC	TGCAGGCGGC	GCAGGCCCGG	CTGGGCGCGG	ACATGGAGGA	60
CGTGTGCGGC	CGCCTGGTGC	AGTACCGCGG	CGAGGTGCAG	GCCATGCTCG	GCCAGAGCAC	120
CGAGGAGCTG	CGGGTGCGCC	TGGCTCCCA	CCTGCGCAAG	CTGCGTAAGC	GGCTCCTCCG	180
CGATGCCGAT	GACCTGCAGA	AGTGCCTGGC	AGTGTACCAG	GCCGGGGCCC	GCGAGGGCGC	240
CGAGCGCGGC	CTC					253

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTISENSE: NO
 (v) FRAGMENT TYPE:
 (vi) ORIGINAL SOURCE:

-280-

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:131:

GAATTACATT CCCAACCGCG TGGCACAACA ACTGGCGGGC AAACAGTCGT TGCTGATT 58

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:132:

ACCATTAAG AAAATATCAT CTTTGSTGTT TCCTATGATG AATATAGAAG CGTCATC 57

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:133:

CTATATTCAT CATAGGAAAC ACCAAAGAT 29

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:134:

CTATATTCAT CATAGGAAAC ACCAAT 26

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

-281-

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

CTATATTCAT CATAGGAAAC ACCAAAGAT

29

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

CTATATTCAT CATAGGAAAC ACCAAAGATG ATATTTTC

38

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

CTATATTCAT CATAGGAAAC ACCAATG ATATTTTC

35

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO

-282-

(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

CTATATTCAT CATAGGAAAC ACCAAAGATA TTTTC

35

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

CTATATTCAT CATAGGAAAC ACCAAAGATG C

31

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 200 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

CTTCCACCGC GATGTTGATG ATTATGTGTC TGAATTTGAT GGGGGCAGGC GGCCCCCGTC
TGTTTGTCGC GGCTCTGGTG TTGATGGTGG TTCTCTGCCT TGTCACCCTC GACCTGCAGC
CCAAGCTTGG GATCCACCAC CATCACCATC ACTAATAATG CATGGGCTGC AGCCAATTGG
CACTGGCCGT CGTTTTACAA

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 99 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

-283-

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GTCACCCCTCG ACCTGCAGCC CAAGCTTGGG ATCCACCACC ATCACCATCA CTAATAATGC
ATGGGCTGCA GCCAATTGGC ACTGGCCGTC GTTTTACAA

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

TGTACGTCAC AACTA

15

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

TGTACGTCAC AACTAC

16

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

TGTACGTCAC AACTACA

17

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

-284-

(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

TGTACGTCAC AACTACAA

18

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

TGTACGTCAC AACTACAAT

19

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

TGTACGTCAC AACTACAATA

20

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO

-285-

- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

TGTACGTCAC AACTACAATA G

21

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

TGTACGTCAC AACTACAATA GG

22

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

TGTACGTCAC AACTACAATA GGC

23

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

TGTACGTCAC AACTACAATA GGCC

24

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(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

TGTACGTCAC AACTACAATA GGCCC

25

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

TGTACGTCAC AACTACAATA GGCCCT

26

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

TGTACGTCAC AACTACAATA GGCCCTG

27

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

-287-

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

TGTACGTCAC AACTACAATA GGCCCTGC

28

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

TGTACGTCAC AACTACAATA GGCCCTGCA

29

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

TGTACGTCAC AACTACAATA GGCCCTGCAC

30

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

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TGTTACGTCAC AACTACAATA GGCCCTGCAC C

31

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

TGTTACGTCAC AACTACAATA GGCCCTGCAC CA

32

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

TGTTACGTCAC AACTACAATA GGCCCTGCAC CAG

33

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

TGTTACGTCAC AACTACAATA GGCCCTGCAC CAGG

34

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid

-289-

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

TGTACGTCAC AACTACAATA GGCCCTGCAC CAGGC

35

- (2) INFORMATION FOR SEQ ID NO:163:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

TGTACGTCAC AACTACAATA GGCCCTGCAC CAGGCC

36

- (2) INFORMATION FOR SEQ ID NO:164:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

TGTACGTCAC AACTACAATA GGCCCTGCAC CAGGCCA

37

- (2) INFORMATION FOR SEQ ID NO:165:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:

-290-

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

TGTACGTCAC AACTACAATA GGCCCTGCAC CAGGCCAG

38

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

TGTACGTCAC AACTACAATA GGCCCTGCAC CAGGCCAGA

39

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

CTGATGCGTC GGATCATCC

19

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

CTGATGCGTC GGATCATCCA

20

(2) INFORMATION FOR SEQ ID NO:169:

-291-

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

CTGATGCGTC GGATCATCCA G

21

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

CTGATGCGTC GGATCATCCA GC

22

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

CTGATGCGTC GGATCATCCA GCA

23

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

-292-

(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

CTGATGCGTC GGATCATCCA GCAG

24

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

CTGATGCGTC GGATCATCCA GCAGC

25

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

CTGATGCGTC GGATCATCCA GCAGCA

26

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

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CTGATGCGTC GGATCATCCA GCAGCAG

27

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

CTGATGCGTC GGATCATCCA GCAGCAGC

28

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

CTGATGCGTC GGATCATCCA GCAGCAGCA

29

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

CTGATGCGTC GGATCATCCA GCAGCAGCAG

30

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid

-294-

(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

CTGATGCGTC GGATCATCCA GCAGCAGCAG C

31

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

CTGATGCGTC GGATCATCCA GCAGCAGCAG CA

32

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

CTGATGCGTC GGATCATCCA GCAGCAGCAG CAG

33

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:

-295-

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

CTGATGCGTC GGATCATCCA GCAGCAGCAG CAGC

34

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

CTGATGCGTC GGATCATCCA GCAGCAGCAG CAGCA

35

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

CTGATGCGTC GGATCATCCA GCAGCAGCAG CAGCAG

36

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

CTGATGCGTC GGATCATCCA GCAGCAGCAG CAGCAGC

37

(2) INFORMATION FOR SEQ ID NO:186:

-296-

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

CTGATGCGTC GGATCATCCA GCAGCAGCAG CAGCAGCA

38

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

CTGATGCGTC GGATCATCCA GCAGCAGCAG CAGCAGCAG

39

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

CTGATGCGTC GGATCATCCA GCAGCAGCAG CAGCAGCAGC

40

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

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(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

CTGATGCGTC GGATCATCCA GCAGCAGCAG CAGCAGCAGC A

41

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

CTGATGCGTC GGATCATCCA GCAGCAGCAG CAGCAGCAGC AG

42

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

CTGATGCGTC GGATCATCCA GCAGCAGCAG CAGCAGCAGC AGT

43

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

-298-

CTGATGCGTC GGATCATCCA GCAGCAGCAG CAGCAGCAGC AGTC

44

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

CTGATGCGTC GGATCATCCA GCAGCAGCAG CAGCAGCAGC AGTCA

45

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

CTGATGCGTC GGATCATCCA GCAGCAGCAG CAGCAGCAGC AGTCAC

46

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

CTGATGCGTC GGATCATCCA GCAGCAGCAG CAGCAGCAGC AGTCACG

47

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid

-299-

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

CTGATGCGTC GGATCATCCA GCAGCAGCAG CAGCAGCAGC AGTCACGC

48

(2) INFORMATION FOR SEQ ID NO:197:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 49 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

CTGATGCGTC GGATCATCCA GCAGCAGCAG CAGCAGCAGC AGTCACGCT

49

(2) INFORMATION FOR SEQ ID NO:198:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

CTGATGCGTC GGATCATCCA GCAGCAGCAG CAGCAGCAGC AGTCACGCTA

50

(2) INFORMATION FOR SEQ ID NO:199:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:

-300-

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

CTGATGCGTC GGATCATCCA GCAGCAGCAG CAGCAGCAGC AGTCACGCTA A

51

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

CTGATGCGTC GGATCATCCA GCAGCAGCAG CAGCAGCAGC AGTCACGCTA AC

52

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

CTGATGCGTC GGATCATCCA GCAGCAGCAG CAGCAGCAGC AGTCACGCTA ACC

53

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

CTGATGCGTC GGATCATCCA GCAGCAGCAG CAGCAGCAGC AGTCACGCTA ACCG

54

(2) INFORMATION FOR SEQ ID NO:203:

-301-

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

CTGATGCGTC GGATCATCCA GCAGCAGCAG CAGCAGCAGC AGTCACGCTA ACCGA

55

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

CTGATGCGTC GGATCATCCA GCAGCAGCAG CAGCAGCAGC AGTCACGCTA ACCGAA

56

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

CTGATGCGTC GGATCATCCA GCAGCAGCAG CAGCAGCAGC AGTCACGCTA ACCGAAT

57

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

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(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

CTGATGCGTC GGATCATCCA GCAGCAGCAG CAGCAGCAGC AGTCACGCTA ACCGAATC 58

(2) INFORMATION FOR SEQ ID NO:207:

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

CTGATGCGTC GGATCATCCA GCAGCAGCAG CAGCAGCAGC AGTCACGCTA ACCGAATCC 59

(2) INFORMATION FOR SEQ ID NO:208:

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

CTGATGCGTC GGATCATCCA GCAGCAGCAG CAGCAGCAGC AGTCACGCTA ACCGAATCCC 60

(2) INFORMATION FOR SEQ ID NO:209:

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

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CTGATGCGTC GGATCATCCA GCAGCAGCAG CAGCAGCAGC AGTCACGCTA ACCGAATCCC 60
T 61

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

CTGATGCGTC GGATCATCCA GCAGCAGCAG CAGCAGCAGC AGTCACGCTA ACCGAATCCC 60
TG 62

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

CTGATGCGTC GGATCATCCA GCAGCAGCAG CAGCAGCAGC AGTCACGCTA ACCGAATCCC 60
TGG 63

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

CTGATGCGTC GGATCATCCA GCAGCAGCAG CAGCAGCAGC AGTCACGCTA ACCGAATCCC 60
TGGT 64

(2) INFORMATION FOR SEQ ID NO:213:

-304-

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

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CTGATGCGTC GGATCATCCA GCAGCAGCAG CAGCAGCAGC AGTCACGCTA ACCGAATCCC 60
TGGTC                                           65
```

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

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CTGATGCGTC GGATCATCCA GCAGCAGCAG CAGCAGCAGC AGTCACGCTA ACCGAATCCC 60
TGGTCA                                           66
```

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

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CTGATGCGTC GGATCATCCA GCAGCAGCAG CAGCAGCAGC AGTCACGCTA ACCGAATCCC 60
TGGTCAG                                           67
```

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

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(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

CTGATGCGTC GGATCATCCA GCAGCAGCAG CAGCAGCAGC AGTCACGCTA ACCGAATCCC 60
TGGTCAGA 68

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

CTGATGCGTC GGATCATCCA GCAGCAGCAG CAGCAGCAGC AGTCACGCTA ACCGAATCCC 60
TGGTCAGAT 69

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

CTGATGCGTC GGATCATCCA GCAGCAGCAG CAGCAGCAGC AGTCACGCTA ACCGAATCCC 60
TGGTCAGATC 70

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO

-306-

- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

CTGATGCGTC GGATCATCCA GCAGCAGCAG CAGCAGCAGC AGTCACGCTA ACCGAATCCC 60
TGGTCAGATC T 71

(2) INFORMATION FOR SEQ ID NO:220:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 72 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

CTGATGCGTC GGATCATCCA GCAGCAGCAG CAGCAGCAGC AGTCACGCTA ACCGAATCCC 60
TGGTCAGATC TT 72

(2) INFORMATION FOR SEQ ID NO:221:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

TGCACCTGAC TCC 13

(2) INFORMATION FOR SEQ ID NO:222:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

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TGCACCTGAC TCCT

14

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

TGCACCTGAC TCCTG

15

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

TGCACCTGAC TCCTGT

16

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

TGCACCTGAC TCCTGTG

17

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid

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- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

TGCACCTGAC TCCTGTGG

18

(2) INFORMATION FOR SEQ ID NO:227:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

TGCACCTGAC TCCTGTGGA

19

(2) INFORMATION FOR SEQ ID NO:228:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

TGCACCTGAC TCCTGTGGAG

20

(2) INFORMATION FOR SEQ ID NO:229:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:

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(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

TGCACCTGAC TCCTGTGGAG A

21

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

TGCACCTGAC TCCTGTGGAG AA

22

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

TGCACCTGAC TCCTGTGGAG AAG

23

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

TGCACCTGAC TCCTGTGGAG AAGT

24

(2) INFORMATION FOR SEQ ID NO:233:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

TGCACCTGAC TCCTGTGGAG AAGTC

25

(2) INFORMATION FOR SEQ ID NO:234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

TGCACCTGAC TCCTGTGGAG AAGTCT

26

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

TGCACCTGAC TCCTGTGGAG AAGTCTG

27

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

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(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

TGCACCTGAC TCCTGTGGAG AAGTCTGC

28

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

TGCACCTGAC TCCTGTGGAG AAGTCTGCC

29

(2) INFORMATION FOR SEQ ID NO:238:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

TGCACCTGAC TCCTGTGGAG AAGTCTGCCG

30

(2) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

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TGCACCTGAC TCCTGTGGAG AAGTCTGCCG T

31

(2) INFORMATION FOR SEQ ID NO:240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:240:

TGCACCTGAC TCCTGTGGAG AAGTCTGCCG TT

32

(2) INFORMATION FOR SEQ ID NO:241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:241:

TGCACCTGAC TCCTGTGGAG AAGTCTGCCG TTA

33

(2) INFORMATION FOR SEQ ID NO:242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:242:

TGCACCTGAC TCCTGTGGAG AAGTCTGCCG TTAC

34

(2) INFORMATION FOR SEQ ID NO:243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid

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- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

TGCACCTGAC TCCTGTGGAG AAGTCTGCCG TTACT

35

(2) INFORMATION FOR SEQ ID NO:244:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

TGCACCTGAC TCCTGTGGAG AAGTCTGCCG TTACTG

36

(2) INFORMATION FOR SEQ ID NO:245:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

TGCACCTGAC TCCTGTGGAG AAGTCTGCCG TTACTGC

37

(2) INFORMATION FOR SEQ ID NO:246:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:

-314-

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

TGCACCTGAC TCCTGTGGAG AAGTCTGCCG TTA CTGCC

38

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

TGCACCTGAC TCCTGTGGAG AAGTCTGCCG TTA CTGCC

39

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

TGCACCTGAC TCCTGTGGAG AAGTCTGCCG TTA CTGCCCT

40

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

TGCACCTGAC TCCTGTGGAG AAGTCTGCCG TTA CTGCCCT G

41

(2) INFORMATION FOR SEQ ID NO:250:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

TGCACCTGAC TCCTGTGGAG AAGTCTGCCG TTAGTCCCCT GT

42

(2) INFORMATION FOR SEQ ID NO:251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

TGCACCTGAC TCCTGTGGAG AAGTCTGCCG TTAGTCCCCT GTG

43

(2) INFORMATION FOR SEQ ID NO:252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

TGCACCTGAC TCCTGTGGAG AAGTCTGCCG TTAGTCCCCT GTGG

44

(2) INFORMATION FOR SEQ ID NO:253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

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- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

TGCACCTGAC TCCTGTGGAG AAGTCTGCCG TTACTGCCCT GTGGG

45

(2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

TGCACCTGAC TCCTGTGGAG AAGTCTGCCG TTACTGCCCT GTGGGG

46

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

TGCACCTGAC TCCTGTGGAG AAGTCTGCCG TTACTGCCCT GTGGGGC

47

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

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TGCACCTGAC TCCTGTGGAG AAGTCTGCCG TTA CTGCCCT GTGGGGCA

48

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

TGCACCTGAC TCCTGTGGAG AAGTCTGCCG TTA CTGCCCT GTGGGGCAA

49

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

TGCACCTGAC TCCTGTGGAG AAGTCTGCCG TTA CTGCCCT GTGGGGCAAG

50

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

TGCACCTGAC TCCTGTGGAG AAGTCTGCCG TTA CTGCCCT GTGGGGCAAG G

51

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid

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- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

TGCACCTGAC TCCTGTGGAG AAGTCTGCCG TTA CTGCCCT GTGGGGCAAG GT 52

- (2) INFORMATION FOR SEQ ID NO:261:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 209 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

CATTTGCTTC TGACACAACCT GTGTTCACTA GCAACCTCAA ACAGACACCA TGGTGCACCT 60
GACTCCTGTG GAGAAGTCTG CCGTTACTGC CCTGTGGGGC AAGGTGAACG TGGATGAACT 120
TGSTGGGTGAG GCCCTGGGCA GGTGGSTATC AAGGTTACAA GACAGGTTTA AGGAGACCAA 180
TAGAAACTGG GCATGTGGAG ACAGAGAAG 209

- (2) INFORMATION FOR SEQ ID NO:262:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 88 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

TGAGACTCTG TCTCAAAAAT AAATAAATAA ATAAATAAAT AAATAAATAA ATAAATAAAT 60
AAATAAATAA GTAAAAAGA AAGAATGC 88

- (2) INFORMATION FOR SEQ ID NO:263:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 54 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

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(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

GTGTGTGTGT GTGTGTGTT TTTTTTAAAC AGGGATTGTT GGAATTATTT GAGA

54

(2) INFORMATION FOR SEQ ID NO:264:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

TTCCCCAAAT CCCTGTTAAA AAC

23

(2) INFORMATION FOR SEQ ID NO:265:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

TTCCCCAAAT CCCTGTTAAA AAAAC

25

(2) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

TTCCCCAAAT CCCTGTTAAA AAAAAAC

27

(2) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

GTAAACGAC CGCCAGTGCC AAGCTTGCAT GCCTGCAGGT CGACTCTAGA GGATCCCCGG 60
GTACCGAGCT CGAATTCGTA ATCATEGTCA TAGCTGTTTC CTG 103

(2) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

GAGTCAGGTG CGCCATGCCT CAAACAGACA CCATGGTGCA CCTGACTCCT GAGGAGNCTG 60
GGCATGTGGA GACAGAGA 73

(2) INFORMATION FOR SEQ ID NO:269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

TTTGTGTCTC CACATGCCCA GNTTCTTCAG GACTCAGGTG CACATGTGT CTSTTTGAGG 60

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CATGGCGCAC CTGAGCTC

78

(2) INFORMATION FOR SEQ ID NO:270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

TCTCTGTCTC CACATGCCCA GCTCCTCAG GAGTCAGGTG CGCCATGGTG TCTGTTTGAG 60
GCATG3CGCA CGTGACTC 78

(2) INFORMATION FOR SEQ ID NO:271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

TCTCTGTCTC CACATGCCCA GCTCCTCAG GAGTCAGGTG CGCCATGGTG TCTGTTTGAG 60
GCATG3CGCA CTGACTCCT GA 82

(2) INFORMATION FOR SEQ ID NO:272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

TCTCTGTCTC CACATGCCCA GCTCCTCAG GAGTCAGGTG CG 42

(2) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:

-322-

- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

CACCTGACTC CTA

13

(2) INFORMATION FOR SEQ ID NO:274:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 14 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

CACCTGACTC CTGGA

14

(2) INFORMATION FOR SEQ ID NO:275:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 14 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

CACCTGACTC CTGA

14

(2) INFORMATION FOR SEQ ID NO:276:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO

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(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

CCATGGGTGTC TGTTTGAGGC ATGGCG

26

(2) INFORMATION FOR SEQ ID NO:277:

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(1i) MOLECULE TYPE: cDNA
(1ii) HYPOTHETICAL: NO
(1v) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

CAGCTCTCAT TTTCATACA GTCAGTATCA ATTCTGGAAG AATTTCCAGA CATTAAAGAT 60
AGTCATCTTG GGGCT 75

(2) INFORMATION FOR SEQ ID NO:278:

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(1i) MOLECULE TYPE: cDNA
(1ii) HYPOTHETICAL: NO
(1v) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

ACCTAGCGTT CAGTTCGACT GAGATAATAC GACTCACTAT AGCAGCTCTC ATTTTCCATA 60
C 61

(2) INFORMATION FOR SEQ ID NO:279:

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(1i) MOLECULE TYPE: RNA
(1ii) HYPOTHETICAL: NO
(1v) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

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GUCACUACAG GUGAGCUCCA

20

(2) INFORMATION FOR SEQ ID NO:280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

CTCAGTCCAC GTGCTACCCT GCTG

24

(2) INFORMATION FOR SEQ ID NO:281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

CATTTGCTTC TGACACAACCT GTGTTCACTA GCAACCTCAA ACAGACACCA TGGTGACACCT
GACTCCTGAG GAGAACTCTG CCGTT

85

(2) INFORMATION FOR SEQ ID NO:282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

ACGGGTCCCG GAGTGGTGTG GC

22

(2) INFORMATION FOR SEQ ID NO:283:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

```
ACTGCCCTGT GGGSCAAGGT GAACGTGGAT GAAGTTGGTG GTGAGGCCCT GGGCAGGTTG 60
GTATCAAGGT TACAAG 76
```

(2) INFORMATION FOR SEQ ID NO:284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

```
ACTGCCCTGT GGGSCAAGGT GAACGTGGAT GAAGTTGGTG GTGAGGCCCT GGGCAGATTG 60
GTATCAAGGT TACAAG 76
```

(2) INFORMATION FOR SEQ ID NO:285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

```
ACTGCCCTGT GGGSCAAGGT GAACGTGGAT GAAGTTGGTG GTGAGGCCCT GGGCAGGTTG 60
CTATCAAGGT TACAAG 76
```

(2) INFORMATION FOR SEQ ID NO:286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

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(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

ACTGCCCTGT GGGGCAAGGT GAACGTGGAT GAAGTTGGTG GTGAGGCCCT GGGCAGGTTG 60
GCATCAAGGT TACAA3 76

(2) INFORMATION FOR SEQ ID NO:287:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH 48 base pairs
(B) TYPE nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

ACAGGTTTAA GGAGACCAAT AGAAACTGGG CATGTGGAGA CAGAGAAG 48

(2) INFORMATION FOR SEQ ID NO:288:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH 24 base pairs
(B) TYPE nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

GACGACGACT GCTACCTGAC TCCA 24

(2) INFORMATION FOR SEQ ID NO:289:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH 24 base pairs
(B) TYPE nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:

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(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

ACAGCGCACT GCTACCTGAC TCCA

24

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

TGGAGTCAGG TAGCAGTC

18

(2) INFORMATION FOR SEQ ID NO:291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

CAGCTCTCAT TTTCCATACA GTCAGTATCA ATTCTGGAAG AATTTCCAGA CATTAAAGAT 60

(2) INFORMATION FOR SEQ ID NO:292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

AGTCATCTTG GGGCTCTCGA GAGTAAAAGG TATGTCAGTC ATAGTTAAGA CCTTCTTAAA
GGTCT

65

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(2) INFORMATION FOR SEQ ID NO:293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

GTAATTTCTA TCAGTAGAAC CCCGA

25

(2) INFORMATION FOR SEQ ID NO:294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

CAGCTCTCAT TTTCATACA CTCAGTATCA ATTCTGGAAG AATTTCCAGA CATTAAAGAT 60

(2) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

AGTCATCTTG GGGCT

15

(2) INFORMATION FOR SEQ ID NO:296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

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(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

CAGCTCTCAT TTTCCATACA GTCAGTATCA ATTCTGGAAG AATTTCCAGA CATTAAAGAT 60

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

AGTCATCTTG GGGCTA

16

(2) INFORMATION FOR SEQ ID NO:298:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

CAGCTCTCAT TTTCCATACA TTAAAGATAG TCATCTTGGG GCT

43

(2) INFORMATION FOR SEQ ID NO:299:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

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CAGCTCTCAT TTTCATACA TTAAAGATAG TCATCTTGGG GCTA

44

(2) INFORMATION FOR SEQ ID NO:300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

CAGCTCTCAT TTTCATACA GT

22

(2) INFORMATION FOR SEQ ID NO:301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

CAGCTCTCAT TTTCATACA T

21

(2) INFORMATION FOR SEQ ID NO:302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

GCCTGGTACA CTGCCAGGCG CTTCTGCAGG TCATCGGCAT CGCGGAGGAG

50

(2) INFORMATION FOR SEQ ID NO:303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid

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- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

GCCTGGTACA CTGCCAGGCA CTTCTGCAGG TCATCGGCAT CGCGGAGGAG

50

- (2) INFORMATION FOR SEQ ID NO:304:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

GATGCCGATG ACCTGCAGAA G

21

- (2) INFORMATION FOR SEQ ID NO:305:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

GATGCCGATG ACCTGCAGAA GC

22

- (2) INFORMATION FOR SEQ ID NO:306:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO

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- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

GATGCCGATG ACCTGCAGAA GTGC

24

(2) INFORMATION FOR SEQ ID NO:307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

GATGATCCGA CG

12

(2) INFORMATION FOR SEQ ID NO:308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

CTGATGCGTC GGATCATC

18

(2) INFORMATION FOR SEQ ID NO:309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

GATGATCCGA CG

12

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(2) INFORMATION FOR SEQ ID NO:310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

GGCGCGGACA TGGAGGACGT GTGCGGCCGC CTGGT

35

(2) INFORMATION FOR SEQ ID NO:311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

TCCGCGATGC CGATGACCTG CAGAAGCGCC TGGC

34

(2) INFORMATION FOR SEQ ID NO:312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

CGGCTGCGAT CACCGTGCGG CACAGCT

27

(2) INFORMATION FOR SEQ ID NO:313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

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(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

CGGCTGCGAT CACCGTGCGG T

21

(2) INFORMATION FOR SEQ ID NO:314:

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

CGGCTGCGAT CACCGTGCGG AACAGCT

27

(2) INFORMATION FOR SEQ ID NO:315:

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

CGGCTGCGAT CACCGTGCGG CA

22

(2) INFORMATION FOR SEQ ID NO:316:

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

CGGCTGCGAT CACCGTGCGG TA

22

(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

CGGCTGCGAT CACCGTGCGG A

21

(2) INFORMATION FOR SEQ ID NO:318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

ATCATCAACT GGAAGATCAG GTCAGGAGCC ACTTGCCANC CT

42

(2) INFORMATION FOR SEQ ID NO:319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

ATCATCACAC TGGAAGACTC CAGGTCAGGA GCC

33

(2) INFORMATION FOR SEQ ID NO:320:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

ATCCACTACA ACTACATGTG TAACAGTTGG WGCwwGCC

48

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WHAT IS CLAIMED IS:

1. A process for determining the sequence of a target nucleic acid molecule comprising the steps of:
 - a) generating at least two nucleic acid fragments from the target nucleic acid; and
 - b) analyzing the at least two fragments by a mass spectrometry format, and thereby determine the sequence of the target nucleic acid molecule.
2. A process of claim 1, wherein in step a), an endonuclease is contacted with the target nucleic acid to generate the at least two nucleic acid fragments.
3. A process of claim 2, wherein the endonuclease is a restriction enzyme that can recognize and cleave at least one restriction site in the target nucleic acid.
4. A process of claim 2, wherein the target nucleic acid is a deoxyribonucleic acid and the nuclease is a deoxyribonuclease.
5. A process of claim 2, wherein the target nucleic acid is a ribonucleic acid and the nuclease is a ribonuclease.
6. A process of claim 5, wherein the ribonuclease is selected from the group consisting of: the G-specific T_1 ribonuclease, the A-specific U_2 ribonuclease, the A/U specific PhyM ribonuclease, the U/C specific ribonuclease A, the C-specific chicken liver ribonuclease and crisavitin.
7. A process of claim 1, wherein in step a), nucleic acid fragments are generated by performance of a combined amplification and base-specific termination reaction.
8. A process of claim 7, wherein the combined amplification and base-specific termination reaction is performed using a first polymerase, which has a relatively low affinity towards at least one chain terminating

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nucleotide and an a second polymerase, which has a relatively high affinity towards at least one chain terminating nucleotide.

9. A process of claim 8, wherein the first and second polymerases are thermostable DNA polymerases.

- 5 10. A process of claim 9, wherein the thermostable DNA polymerases are selected from the group consisting of: Taq DNA polymerase, AmpliTaq FS DNA polymerase, Deep Vent (exo-) DNA polymerase, Vent DNA polymerase, Vent (exo-) DNA polymerase, Vent DNA polymerase, Vent (exo-) DNA polymerase, Deep Vent DNA polymerase, Thermo Sequenase, *exo(-) Pseudococcus furiosus (Pfu)* DNA polymerase, AmpliTaq, Ultman, 9 degree Nm, Tth, Hot Tub, *Pyrococcus furiosus (Pfu)* and *Pyrococcus woesei (Pwo)* DNA polymerase.

11. A process of claim 1, wherein the at least two nucleic acid fragments generated in step a) include mass modified nucleotides.

- 15 12. A process of claim 1, wherein the at least two fragments comprise a 3' tag.

13. A process of claim 1, wherein the at least two fragments comprise a 5' tag.

- 20 14. A process of claim 12 or 13, wherein the tag is a non-natural tag.

15. A process of claim 14, wherein the non-natural tag is selected from the group consisting of: an affinity tag and a mass marker.

16. A process of claim 15, wherein the affinity tag facilitates immobilization of the nucleic acid to a solid support.

- 25 17. A process of claim 16, wherein the affinity tag is biotin or a nucleic acid sequence that is capable of binding to a capture nucleic acid sequence that is bound to a solid support.

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18. A process of claim 1, wherein the process additionally comprises the step of: ordering the at least two nucleic acid fragments to determine the sequence of the target nucleic acid.

19. A process for detecting a target nucleic acid present in a
5 biological sample, comprising the steps of:
- a) performing on a nucleic acid obtained from a biological sample; a first polymerase chain reaction using a first set of primers, which are capable of amplifying a portion of the nucleic acid containing the target nucleic acid, thereby producing a first amplification
10 product; and
 - b) detecting the first amplification product by mass spectrometry, wherein detection of the target nucleic acid indicates that the target nucleic acid is present in the biological sample.

20. A process of claim 19, wherein prior to step b), a second
15 polymerase chain reaction is performed on the first amplification product using a second set of primers, which are capable of amplifying at least a portion of the first amplification product, which contains the target nucleic acid.

21. A process of claim 19 or 20, wherein prior to step b), the
20 target nucleic acid is immobilized to a solid support.

22. A process of claim 21, wherein the target nucleic acid is reversibly immobilized.

23. A process of claim 22, wherein the target nucleic acid can be
cleaved from the solid support by a chemical, enzymatic or physical
25 process.

24. A process of claim 23, wherein immobilization is accomplished via a photocleavable bond.

25. A process of claim 22, wherein the target nucleic acid is cleaved from the support during step b).

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26. A process of claim 21, wherein the solid support is selected from the group consisting of: beads, flat surfaces, chips, capillaries, pins, combs and wafers.

27. A process of claim 21, wherein immobilization is
5 accomplished by hybridization between a complementary capture nucleic acid molecule immobilized to a solid support, and a portion of the nucleic acid molecule, which is distinct from the target nucleic acid sequence.

28. A process of claim 19 or 20, wherein prior to step b), the target nucleic acid is purified.

10 29. A process of claim 19 or 20, wherein the primer or first or second amplification product is conditioned.

30. A process of claim 29, wherein the primer or first or second amplification product is conditioned by phosphodiester backbone modification.

15 31. A process of claim 30, wherein the phosphodiester backbone modification is a cation exchange.

32. A process of claim 29, wherein the primer or first or second amplification product is conditioned by contact with an alkylating agent or trialkylsilyl chloride.

20 33. A process of claim 29, wherein conditioning is effected by including at least one nucleotide that reduces sensitivity for depurination in the primer or first or second amplification product.

34. A process of claim 33, wherein the nucleotide is an N7- or N9- deazapurine nucleotide or 2' fluoro 2' deoxy nucleotide.

25 35. A method for detecting neoplasia/malignancies in a tissue or cell sample, comprising detecting telomerase activity, mutation of a proto-oncogene, expression of a tumor specific gene in the sample by detecting nucleic acids that encode the telomerase, that are specific for the mutation or that encode the tumor-specific by mass spectrometry.

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36. The method of claim 35 that is a method for detecting neoplasia/malagnancies in a tissue or cell sample, comprising:

- 5
- a) isolating telomerase from the sample and adding a synthetic DNA primer, which is optionally immobilized, complementary to a telomeric repeat, and all four deoxynucleotide triphosphates under conditions that result in telomerase specific extension of the synthetic DNA;
- 10
- b) amplifying the telomerase extended DNA product; and
- c) detecting the DNA product by mass spectrometry, wherein telomerase-specific extension is indicative of neoplasia/malignancy.

37. The method of claim 36, wherein the primer contains a linker moiety for immobilization on a support; and the amplified primers are isolated conjugating the linker portion to a solid support.

38. The method of claim 35 that is a method for identifying transformed cells or tissues, comprising:

- 20
- a) in a cell or tissue sample, amplifying a portion of a proto-oncogene that includes a codon indicative of transformation, wherein one primer comprises a linker moiety for immobilization;
- c) immobilizing DNA via the linker moiety to a solid support, optionally in the form of an array;
- 25
- d) hybridizing a primer complementary to the proto oncogene sequence that is upstream from the codon
- e) adding 3dNTPs/1 ddNTP and DNA polymerase and extending the hybridized primer to the next ddNTP location;

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- f) ionizing/volatizing the sample; and
- g) detecting the mass of the extended DNA, whereby mass indicates the presence of wild-type or mutant alleles. The presence of a mutant allele at the codon

5

is diagnostic for neoplasia.

39. The method of claim 38, wherein the proto-oncogene is the RET-proto-oncogene.

40. The method of claim 35 that is a method for detecting expression of a tumor-specific gene, comprising:

10

- a) isolating polyA RNA from the sample;
- c) preparing a cDNA library using reverse transcription;
- d) amplifying a cDNA product, or portion thereof, of the tumor-specific gene, wherein one oligo primer comprises a linker moiety;

15

- e) isolating the amplified product by immobilizing the DNA to a solid support via the linker moiety;
- f) optionally conditioning the DNA;
- g) ionizing/volatizing sample and detecting the presence

of a DNA peak that is indicative of expression of the gene.

20

41. The method of claim 40, wherein the cells are bone marrow cells, the gene is the tyrosine hydroxylase gene, and expression of the gene is indicative of neuroblastoma.

42. A method for directly detecting a double-stranded nucleic acid using matrix-assisted laser desorption/ionization (MALDI)-time-of-flight (TOF) mass spectrometry, comprising:

25

- a) isolating a double-stranded DNA fragment from a cell or tissue sample;

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- 5 b) preparing the double-stranded DNA for analysis under conditions that increase the ratio of dsDNA:ssDNA, wherein the conditions include one or all of the following: preparing samples for analysis at reduced temperatures (i.e. 4 ° C), and using of higher DNA concentrations in the matrix to drive duplex formation;
- c) ionizing/volatizing the sample of step b), wherein low acceleration voltage of the ions are used;
- d) detecting the presence of the double-stranded DNA.
- 10 43. A method for comparing DNA samples to discern relatedness or to detect mutations, comprising:
- a) obtaining biological a plurality of samples;
- b) amplifying a region of DNA from each sample that contains two or more microsatellite DNA repeat sequences;
- 15 c) ionizing/volatizing the amplified DNA;
- d) detecting the presence of the amplified DNA and comparing the molecular weight of the amplified DNA, wherein different sizes are indicative of non-identity between or among the samples.
- 20 44. The method of claim 43, wherein non-identity is indicative of the presence of a mutation in the DNA in one sample, non-relatedness or non-HLA compatibility between or among the individuals from whom the samples were obtained.
45. The method of claim 43 or 44, wherein a plurality of
- 25 markers are examined simultaneously.

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46. A method for detecting a target nucleic acid in a sample, comprising:

- a) amplifying a target nucleic acid sequence using;
 - (i) a first primer, wherein:
 - 5 the 5'-end shares identity to a portion of the target DNA immediately downstream from the targeted codon followed by a sequence that introduces a unique restriction endonuclease site, and
 - the 3'-end primer is self-complementary; and
 - 10 (ii) a second downstream primer that contains a tag;
- b) immobilizing the double-stranded amplified DNA to a solid support via the linker moiety;
- c) denaturing the immobilized DNA and isolating the non-immobilized DNA strand;
- 15 d) annealing the intracomplementary sequences in the 3'-end of the isolated non-immobilized DNA strand, such that the 3'-end is extendable by a polymerase;
- f) extending the annealed DNA by adding DNA polymerase, 3 dNTPs/1 ddNTP;
- 20 g) cleaving the extended double stranded stem loop DNA with the unique restriction endonuclease and removing the cleaved stem loop DNA;
- i) ionizing/volatizing the extended product; and
- j) detecting the presence of the extended target nucleic acid, where
25 by the presence of a DNA fragment of a mass different from wild-type is indicative of a mutation at the target codon(s).

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47. A method for detecting a target nucleic acid in a biological sample using RNA amplification, comprising:

amplifying the target nucleic acid using a primer comprising a region complementary to the target sequence and a region that encodes

5 a promoter;

synthesizing RNA using an RNA polymerase that recognizes the promoter;

detecting the resulting RNA using mass spectrometry.

48. A primer for mass spectrometric analyses, comprising all or

10 at least about 20, preferably about 16, bases of any of the sequence of nucleotide sequences set forth in SEQ ID NOs. 1-22, 24, 27-38, 41-86, 89, 92, 95, 98, 101-110, 112-123, 126, 128 and 129, wherein the primer is unlabeled.

49. The primer of claim 48, further comprising a mass

15 modifying moiety.

50. A process for detecting a target nucleic acid sequence present in a biological sample, comprising the steps of:

a) obtaining a nucleic acid molecule containing a target nucleic acid sequence from a biological sample;

20 b) immobilizing the target sequence on the support via thiol linkages, whereby the target is present at a sufficient density to detect it using mass spectrometry;

c) hybridizing a detector oligonucleotide with the target nucleic acid sequence;

25 d) removing unhybridized detector oligonucleotide;

e) ionizing and volatilizing the product of step c); and

f) detecting the detector oligonucleotide by mass spectrometry, wherein detection of the detector oligonucleotide indicates the presence of the target nucleic acid sequence in the biological sample.

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51. The process of claim 50, wherein the target nucleic acid molecule is amplified prior to immobilization.

52. The process of claim 50 or 52, wherein at least one of the detector oligonucleotide or the target nucleic acid sequence has been
5 conditioned.

53. A process of any of claims 50-52, wherein the solid support is selected from the group consisting of: beads, flat surfaces, pins and combs.

54. A process of any of claims 50-53, wherein target nucleic
10 acid is immobilized in the form of an array.

55. A process of any of claims 50-54, wherein the support is a silicon wafer.

56. A process of any of claims 51-55, wherein the target nucleic acid molecule is amplified by an amplification procedure selected
15 from the group consisting of cloning, transcription, the polymerase chain reaction (PCR), the ligase chain reaction (LCR), and strand displacement amplification (SDA).

57. A process of any of claims 50-56, wherein the mass spectrometer is selected from the group consisting of: Matrix-Assisted
20 Laser Desorption/Ionization Time-of-Flight (MALDI-TOF), Electrospray (ES), Ion Cyclotron Resonance (ICR), and Fourier Transform.

58. A process of any of claims 50-57, wherein the sample is conditioned by mass differentiating at least two detector oligonucleotides or oligonucleotide mimetics to detect and distinguish at least two target
25 nucleic acid sequences simultaneously.

59. A process of claim 58, wherein the mass differentiation is achieved by differences in the length or sequence of the at least two oligonucleotides.

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60. A process of claim 59, wherein the mass differentiation is achieved by the introduction of mass modifying functionalities in the base, sugar or phosphate moiety of the detector oligonucleotides.

61. A process of claim 58, wherein the mass differentiation is
5 achieved by exchange of cations at the phosphodiester bond.

62. A process of any of claims 50-61, wherein the nucleic acid molecule obtained from a biological sample is amplified into DNA using mass modified dideoxynucleoside triphosphates and DNA dependent DNA polymerase prior to mass spectrometric detection.

10 63. A process of any of claims 50-62, wherein the nucleic acid molecule obtained from a biological sample is amplified into RNA using mass modified ribonucleoside triphosphates and DNA dependent RNA polymerase prior to mass spectrometric detection.

64. A process of any of claims 50-63, herein the target nucleic
15 acid sequence is indicative of a disease or condition selected from the group consisting of a genetic disease, a chromosomal abnormality, a genetic predisposition, a viral infection, a fungal infection and a bacterial infection.

65. A method of determining a sequence of a nucleic acid,
20 comprising the steps of:

- (i) obtaining multiple copies of the nucleic acid to be sequenced;
- (ii) cleaving the multiple copies from a first end to a second end with an exonuclease to sequentially release individual nucleotides;
- (iii) identifying each of the sequentially released nucleotides by
25 mass spectrometry; and
- (iv) determining the sequence of the nucleic acid from the identified nucleotides, wherein the nucleic acid is immobilized by covalent attachment to a solid support via at least one sulfur atom.

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66. A method of determining a sequence of a nucleic acid, comprising the steps of:

- (i) obtaining multiple copies of the nucleic acid to be sequenced;
- (ii) cleaving the multiple copies from a first end to a second end
- 5 with an exonuclease to produce multiple sets of nested nucleic acid fragments;
- (iii) determining the molecular weight value of each one of the sets of nucleic acid fragments by mass spectrometry; and
- (iv) determining the sequence of the nucleic acid from the
- 10 molecular weight values of the sets of nucleic acid fragments, wherein the nucleic acid is immobilized by covalent attachment to a solid support via at least one sulfur atom.

67. The process of claim 65 or 66, wherein the nucleic acids are covalently bound to a surface of the support at a density of at least 20

15 fmol/mm².

68. The method of any of claims 50-67, wherein immobilization is effected by a method comprising:

- reacting a thiol-containing insoluble support with a nucleic acid comprising a thiol-reactive group under conditions such that a covalent
- 20 bond is formed;
- thereby immobilizing the nucleic acid on the insoluble support.

69. The method of claim 68, further including the step of modifying the insoluble support with a thiol-containing reagent, to form a thiol-containing insoluble support.

25 70. The method of claim 68 or 69, wherein the thiol-reactive cross-linking reagent is N-succinimidyl (4-iodoacetyl) aminobenzoate (SIAB).

71. The method of claim 65 or claim 66, wherein the nucleic acid is a 2'-deoxyribonucleic acid (DNA).

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72. The method of claim 65 or claim 66, wherein the nucleic acid is a ribonucleic acid (RNA).

73. The method of any of claims 65-71, wherein the exonuclease is selected from the group consisting of snake venom
5 phosphodiesterase, spleen phosphodiesterase, Bal-31 nuclease, *E. coli* exonuclease I, *E. coli* exonuclease VII, Mung Bean Nuclease, S1 Nuclease, an exonuclease activity of *E. coli* DNA polymerase 1, an exonuclease activity of a Klenow fragment of DNA polymerase 1, an exonuclease activity of T4 DNA polymerase, an exonuclease activity of
10 T7 DNA polymerase, an exonuclease activity of Taq DNA polymerase, an exonuclease activity of DEEP VENT DNA polymerase, *E. coli* exonuclease III, lambda exonuclease and an exonuclease activity of VENT_RDNA polymerase.

74. The method of any of claims 65-74, wherein the nucleic acid
15 comprises mass-modified nucleotides.

75. The method of claim 74, wherein the mass-modified nucleotides modulate the rate of the exonuclease activity.

76. The method of claim 74, wherein the sequentially released nucleotides are mass-modified subsequent to exonuclease release and
20 prior to mass spectrometric identification.

77. The method of claim 76, wherein the sequentially released nucleotides are mass-modified by contact with an alkaline phosphatase.

78. A method of any of claims 65-77, wherein the mass spectrometry format is matrix assisted laser desorption (MALDI) mass
25 spectrometry or electrospray (ES) mass spectrometry.

79. A method of any of claims 65-79, wherein immobilization is effected by a method, comprising:

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reacting the surface of the substrate with a solution of 3-aminopropyltriethoxysilane to produce a uniform layer of primary amines on the surface of the substrate; and

derivatizing the surface of a substrate with iodoacetamido
5 functionalities by reacting the uniform layer of primary amines with a solution of N-succinimidyl (4-iodoacetyl) aminobenzoate (SIAB).

80. A primer, comprising all least about 20, preferably about 16, bases of any of the sequence of nucleotides sequences set forth in SEQ ID NOs. 1-22, 24, 27-38, 41-86, 89, 92, 95, 98, 101-110, 112-123,
10 126, 128 and 129.

81. The primers of claim 80 that is unlabeled, and optionally includes a mass modifying moiety, which is preferably attached to the 5' end.

82. The method of any of claims 1-79, wherein nucleic acid is
15 immobilized to a solid support via a selectively cleavable linker.

83. The method of claim 82, wherein the linker is thermocleavable, enzymatically cleavable, photocleavable or chemically cleavable.

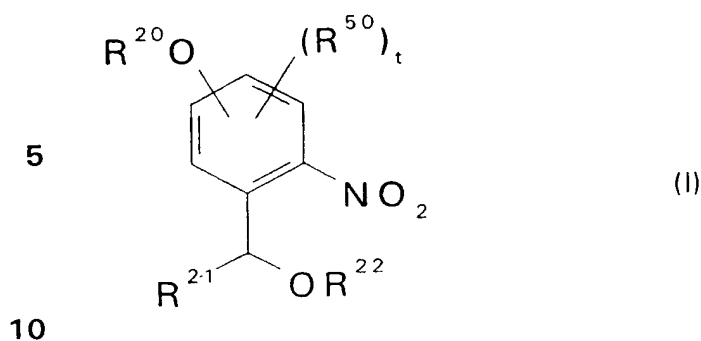
82. The method of claim 82, wherein the linker is a trityl linker.
20

83. The method of claim 82, wherein the linker is selected from the group consisting of 1-(2-nitro-5-(3-O-4,4'-dimethoxytritylpropoxy)-phenyl)-1-O-((2-cyanoethoxy)-diisopropylaminophosphino)ethane and 1-(4-(3-O-4,4'-dimethoxytritylpropoxy)-3-methoxy-6-nitrophenyl)-1-O-((2-cyanoethoxy)-diisopropylaminophosphino)ethane.

25 84. A photolabile linker, comprising a compound of formula:

30

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wherein:

R^{20} is selected from the group consisting of ω -(4,4'-dimethoxytrityloxy)alkyl and ω -hydroxyalkyl;

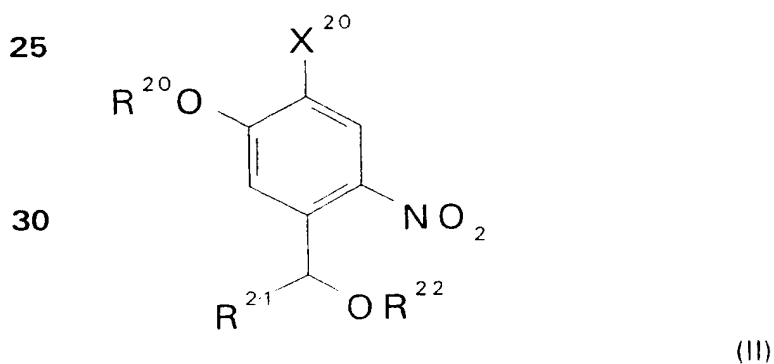
15 R^{21} is selected from the group consisting of hydrogen, alkyl, aryl, alkoxycarbonyl, aryloxycarbonyl and carboxy;

R^{22} is selected from the group consisting of hydrogen and (dialkylamino)(ω -cyanoalkoxy)P-;

t is 0-3; and

20 R^{50} is selected from the group consisting of alkyl, alkoxy, aryl and aryloxy.

85. The photocleavable linker of claim 84, wherein the linkers are of formula II:



35

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wherein:

R^{20} is selected from the group consisting of ω -(4,4'-dimethoxytrityloxy)alkyl, ω -hydroxyalkyl and alkyl;

5 R^{21} is selected from the group consisting of hydrogen, alkyl, aryl, alkoxycarbonyl, aryloxycarbonyl and carboxy;

R^{22} is selected from the group consisting of hydrogen and (dialkylamino)(ω -cyanoalkoxy)P-; and

10 X^{20} is selected from the group consisting of hydrogen, alkyl or OR²⁰.

86. The photocleavable linker of claim 85, wherein:

R^{20} is selected from the group consisting of 3-(4,4'-dimethoxytrityloxy)propyl, 3-hydroxypropyl and methyl;

15 R^{21} is selected from the group consisting of hydrogen, methyl and carboxy;

R^{22} is selected from the group consisting of hydrogen and (diisopropylamino)(2-cyanoethoxy)P-; and

X^{20} is selected from the group consisting of hydrogen, methyl or OR²⁰.

20 87. The photocleavable linker of claim 85, wherein:

R^{20} is 3-(4,4'-dimethoxytrityloxy)propyl;

R^{21} is methyl;

R^{22} is (diisopropylamino)(2-cyanoethoxy)P-; and

X^{20} is hydrogen.

25 88. The photocleavable linker of claim 86, wherein:

R^{20} is methyl;

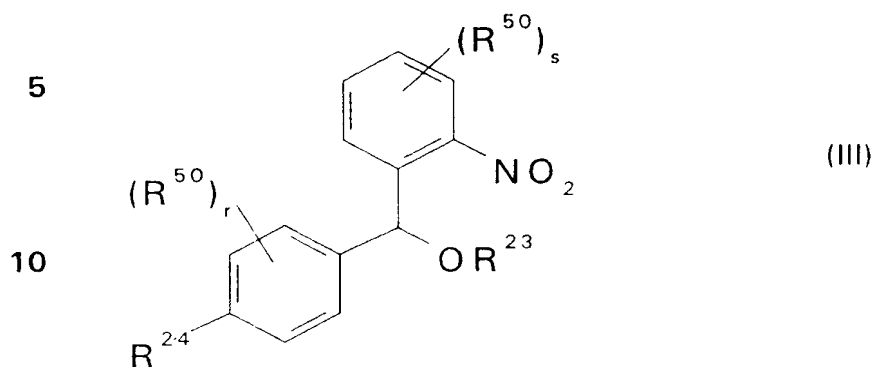
R^{21} is methyl;

R^{22} is (diisopropylamino)(2-cyanoethoxy)P-; and

X^{20} is 3-(4,4'-dimethoxytrityloxy)propoxy.

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88. A photocleavable linker, comprising a compound of formula III:



15 wherein:

R^{23} is selected from the group consisting of hydrogen and (dialkylamino)(ω -cyanoalkoxy)P-;

R^{24} is selected from ω -hydroxyalkoxy, ω -(4,4'-dimethoxytrityloxy)alkoxy, ω -hydroxyalkyl and ω -(4,4'-dimethoxytrityloxy)alkyl, and is unsubstituted or substituted on the alkyl or alkoxy chain with one or more alkyl groups;

r and s are each independently 0-4; and

R^{50} is alkyl, alkoxy, aryl or aryloxy.

89. The photocleavable linker of claim 88, wherein:

25 R^{24} is ω -hydroxyalkyl or ω -(4,4'-dimethoxytrityloxy)alkyl, and is substituted on the alkyl chain with a methyl group.

90. The photocleavable linker of claim 88, wherein:

R^{23} is selected from the group consisting of hydrogen and (diisopropylamino)(2-cyanoethoxy)P-; and

30 R^{24} is selected from the group consisting of 3-hydroxypropoxy, 3-(4,4'-dimethoxytrityloxy)propoxy, 4-hydroxybutyl, 3-hydroxy-1-propyl, 1-hydroxy-2-propyl, 3-hydroxy-2-methyl-1-propyl, 2-hydroxyethyl, hydroxymethyl, 4-(4,4'-dimethoxytrityloxy)butyl, 3-(4,4'-

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dimethoxytrityloxy)-1-propyl, 2-(4,4'-dimethoxytrityloxy)ethyl, 1-(4,4'-dimethoxytrityloxy)-2-propyl, 3-(4,4'-dimethoxytrityloxy)-2-methyl-1-propyl and 4,4'-dimethoxytrityloxymethyl.

91. The photocleavable linker of claim 90, wherein r and s are
5 both 0.

92. The photocleavable linker of claim 91, wherein:

R^{23} is (diisopropylamino)(2-cyanoethoxy)P-; and

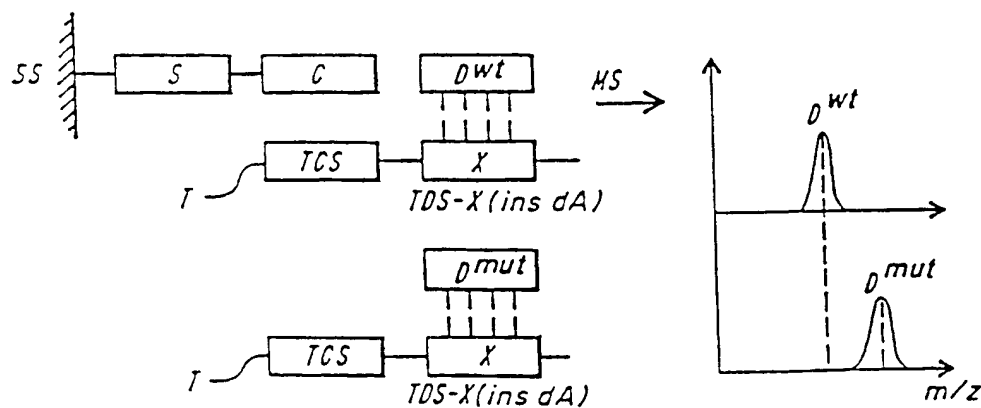
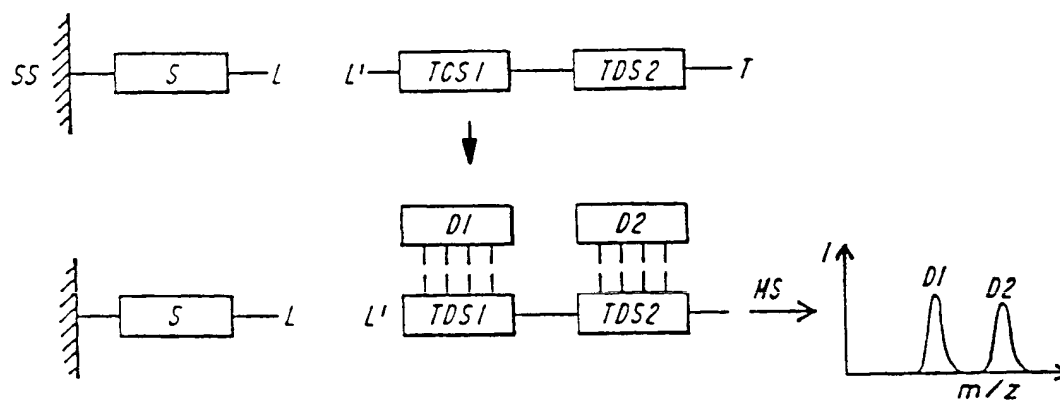
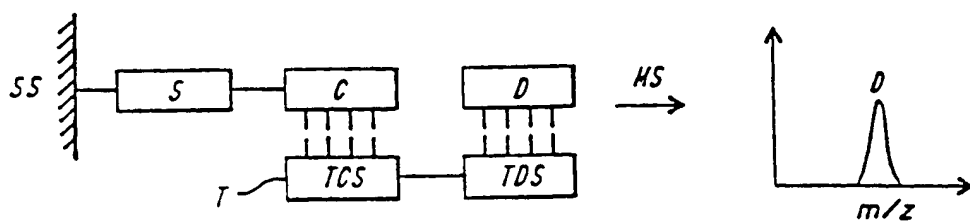
R^{24} is selected from the group consisting of 3-(4,4'-dimethoxytrityloxy)propoxy, 4-(4,4'-dimethoxytrityloxy)butyl, 3-(4,4'-dimethoxytrityloxy)propyl, 2-(4,4'-dimethoxytrityloxy)ethyl, 1-(4,4'-dimethoxytrityloxy)-2-propyl, 3-(4,4'-dimethoxytrityloxy)-2-methyl-1-propyl and 4,4'-dimethoxytrityloxymethyl.
10

93. The photocleavable linker of claim 92, wherein:

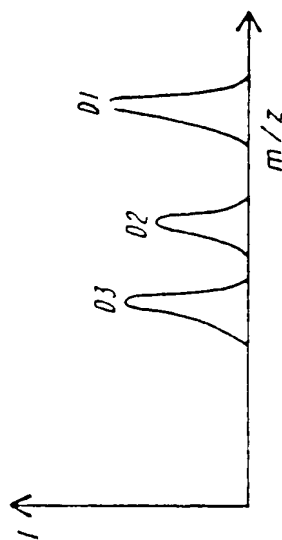
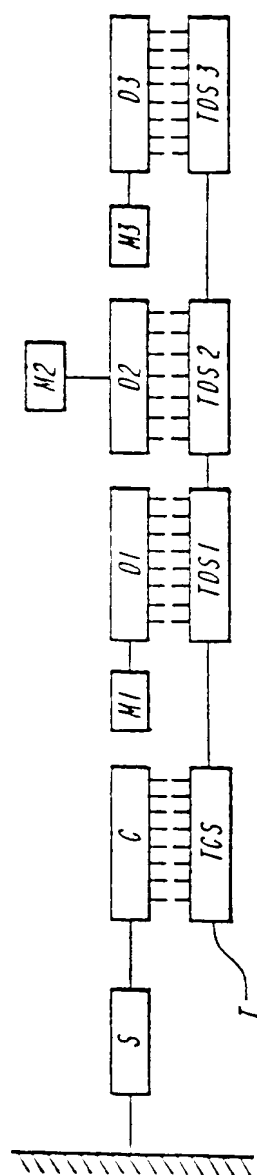
R^{24} is 3-(4,4'-dimethoxytrityloxy)propoxy.

94. The photocleavable linker of claim 84, where in the linker is
15 selected from the group consisting of 1-(2-nitro-5-(3-O-4,4'-dimethoxytritylpropoxy)phenyl)-1-O-((2-cyanoethoxy)-diisopropylaminophosphino)ethane and 1-(4-(3-O-4,4'-dimethoxytritylpropoxy)-3-methoxy-6-nitrophenyl)-1-O-((2-cyanoethoxy)-diisopropylaminophosphino)ethane.

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$I = \text{INTENSITY}$
 $m/z = \frac{\text{MASS}}{\text{CHARGE}}$

$H1 > H2 > H3$

$D1 - D3$ SIMILAR MOLECULAR WEIGHT

H : MASS-MODIFYING FUNCTION

—: POLYMERIC SUPPORT

FIG. 2

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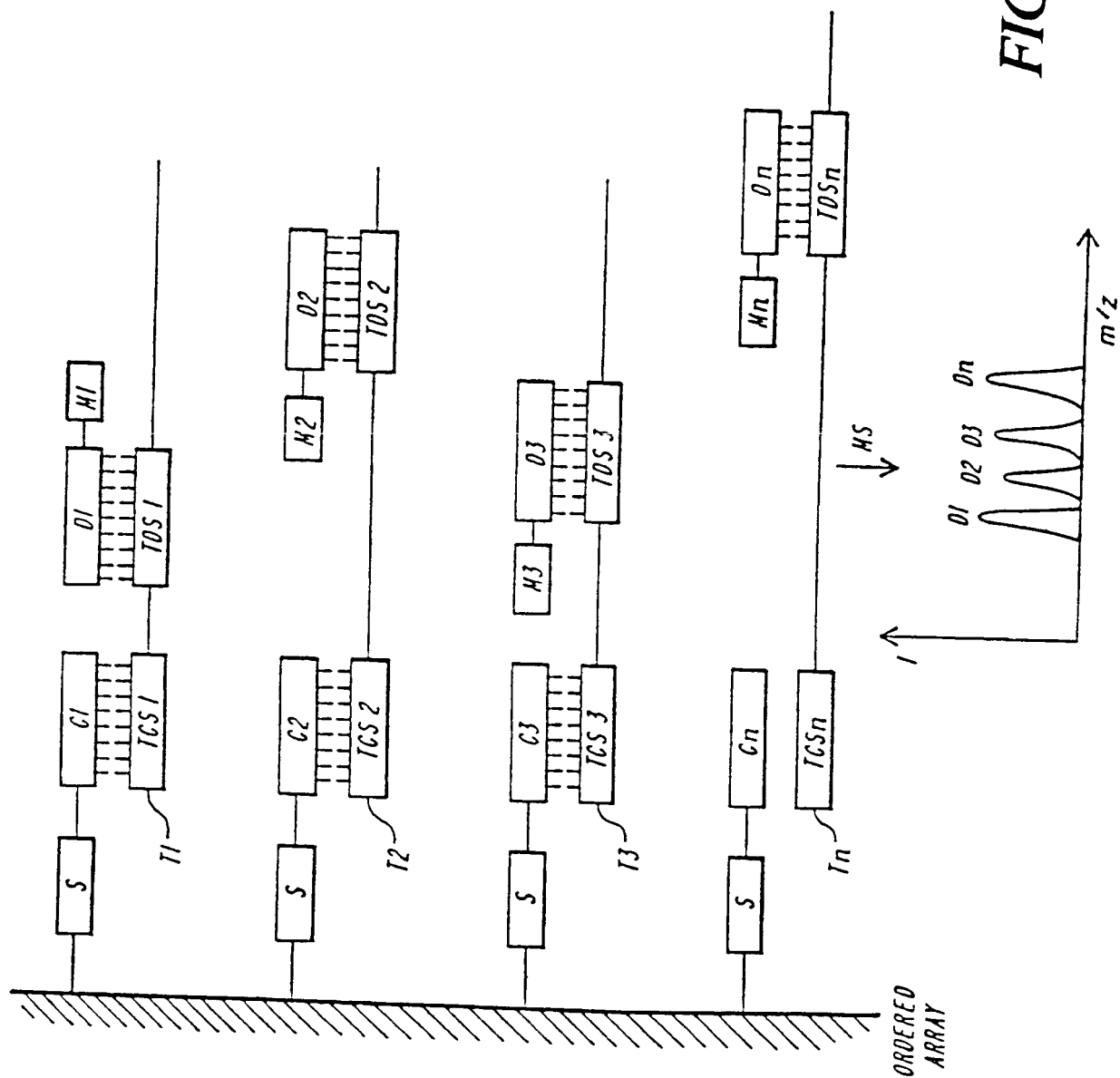


FIG. 3

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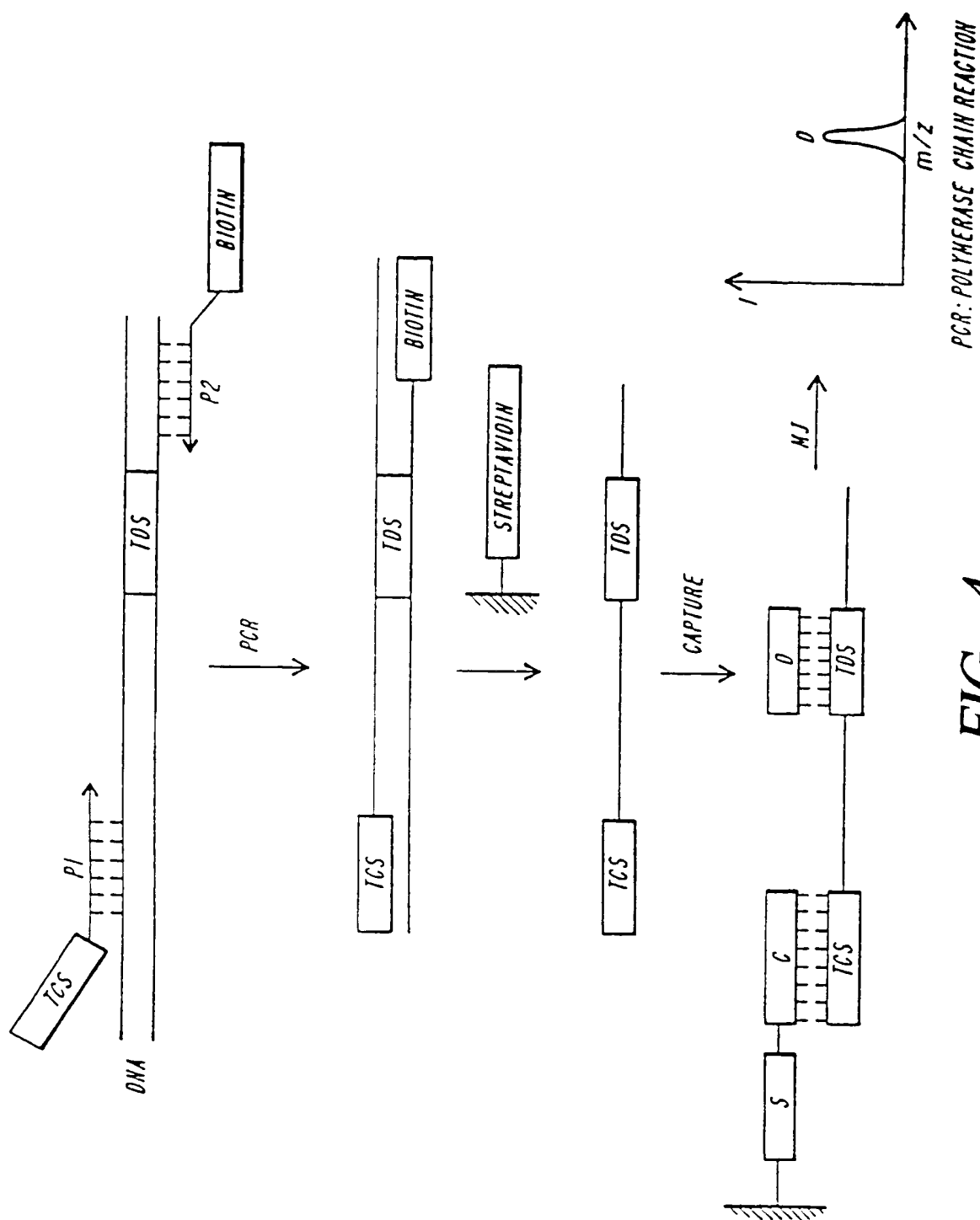


FIG. 4